



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140730

To: Sarvamangala Devi
Location: REM 3C18
Art Unit: 1645
Monday, December 20, 2004

Case Serial Number: 10/696544

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Shears, Beverly

140730

From: Devi, Sarvamangala
Sent: Thursday, December 16, 2004 9:46 AM
To: Shears, Beverly
Subject: 10/696,544

Good morning Beverly:

Please perform a sequence search for SEQ ID NO: 2 ~~both~~ in commercial and interference databases in application 10/696,544. Please include an inventors' name search for Anthony W. Confer; Sahlu Ayalew; George L. Murphy; and Karamjeet Pandher.

Thanx.

S. DEVI, Ph.D.
Primary Examiner
AU 1645
Rems - 3C18



Date completed:

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

____ STIC

____ CM-1

____ Pre-S

Type of Search

____ N.A. Sequence

____ A.A. Sequence

____ Structure

____ Bibliographic

Vendors

____ IC

____ STN

____ Dialog

____ APS

____ Geninfo

____ SDC

____ DARC/Questel

☒ Other CGN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 15:52:32 ; Search time 221.711 Seconds
(without alignments)
874.569 Million cell updates/sec

Title: US-10-696-544-2

Perfect score: 1734

Sequence: 1 CGSGSGSGSSSTPNHPKPVL.....YLIGAKSDNQAIMVSEKK 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1734	100.0	356	2 Q9ZHK7	Q9ZHK7 pasteurella
2	270	15.6	348	2 Q9CKT8	Q9CKT8 pasteurella
3	221.5	12.8	335	2 Q9CKT9	Q9CKT9 pasteurella
4	177	10.2	1158	2 Q6J5M4	Q6J5M4 streptococc
5	177	10.2	1158	2 AAT10376	AAT10376 streptoco
6	174	10.0	331	2 Q9CKU2	Q9CKU2 pasteurella
7	173	10.0	1083	2 Q75W84	Q75W84 streptococc
8	173	10.0	1083	2 BAC98831	BAC98831 streptoco
9	173	10.0	1134	2 Q99051	Q99051 streptococc
10	173	10.0	1164	1 BAG_STRAG	P27951 streptococc
11	172	9.9	1443	2 Q8T1B6	Q8T1B6 dictyosteli
12	171.5	9.9	201	2 O15691	O15691 plasmodium
13	162	9.3	405	2 Q8BMN8	Q8BMN8 mus musculu
14	162	9.3	761	2 Q8ZP12	Q8ZP12 mus musculu
15	162	9.3	761	2 BAC98253	BAC98253 mus muscu
16	162	9.3	883	2 Q8HLB7	Q8HLB7 mus musculu
17	160.5	9.3	365	2 Q9RCG1	Q9RCG1 actinobacil
18	159.5	9.2	365	1 OMLA_ACTPL	Q02937 actinobacil
19	159.5	9.2	365	2 Q9R3L8	Q9R3L8 actinobacil
20	159.5	9.2	896	2 P91448	P91448 caenorhabdi
21	155	8.9	375	2 Q9RCG2	Q9RCG2 actinobacil
22	149	8.6	194	2 O15687	O15687 plasmodium
23	147.5	8.5	364	2 Q9R3S1	Q9R3S1 actinobacil
24	147	8.5	368	2 Q9RCG3	Q9RCG3 actinobacil
25	147	8.5	368	2 Q9RIH8	Q9RIH8 actinobacil
26	147	8.5	837	2 Q9VYV7	Q9VYV7 drosophila
27	143.5	8.3	213	2 Q9VSU1	Q9VSU1 streptococc
28	143.5	8.3	365	2 Q9R3V2	Q9R3V2 actinobacil
29	143	8.2	1364	2 Q8T245	Q8T245 dictyosteli
30	142.5	8.2	677	1 BACS_BOMMO	Q9B1J6 bombyx mori
31	141	8.1	3164	1 T8GU_HHV11	P10220 human herpe

32 140.5 8.1 730 2 Q9X6U0
33 140 8.1 219 2 Q7X576
34 139 8.0 249 2 Q7X579
35 139 8.0 255 2 Q7X578
36 139 8.0 1309 2 Q6CCD1
37 138.5 8.0 201 2 Q7X584
38 138.5 8.0 366 2 Q44163
39 138.5 8.0 367 2 Q44164
40 138.5 8.0 367 2 Q9ZAP9
41 137.5 7.9 201 2 Q8V8U5
42 137 7.9 249 2 Q8V8T7
43 136 7.8 219 2 Q7X580
44 136 7.8 379 2 Q95WF2
45 135.5 7.8 165 2 Q8GAP7

ALIGNMENTS

RESULT 1

Q9ZHK7

ID Q9ZHK7 PRELIMINARY; PRT; 356 AA.
AC Q9ZHK7;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Outer membrane lipoprotein PipE.
GN Name=plpE;
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RV [1]
RP SEQUENCE FROM N.A.
RC STRAIN=89010807N;
RX MEDLINE=99043883; PubMed=9826333;
RA Pandher K., Confer A.W., Murphy G.L.;
RT "Genetic and immunologic analyses of PipE, a lipoprotein important in complement-mediated killing of Pasteurella haemolytica serotype 1.";
RL Infect. Immun. 66:5613-5619 (1998).
DR EMBL; AF059036; AAC82640.1;
DR InterPro; IPR005014; Lipoprotein_14.
DR Pfam; PF03346; Lipoprotein_14; 1.
KW Lipoprotein.
SQ SEQUENCE 356 AA; 39129 MW; E66E48DFE87393D7 CRC64;

Query Match 100.0%; Score 1734; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGSGSGSGSSSTPNHPKPVLPVPTQNNLQANVPQANASQANAPQANAPQV 60
DB 20 CGSGSGSGSSSTPNHPKPVLPVPTQNNLQANVPQANASQANAPQANAPQV 79
QY 61 ENAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQV 120
DB 80 ENAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQV 139
QY 121 KLGTTPPKPKVSGKKIIEEKDFVLNLSQANQANAPQANAPQANAPQV 180
DB 140 KLGTTPPKPKVSGKKIIEEKDFVLNLSQANQANAPQANAPQANAPQV 199
QY 181 VDADKTSOYFVWYDEKRVNDNSDKLTATYRKKEGVPVGSNPHTEFAARISKLGDVEI 240
DB 200 VDADKTSOYFVWYDEKRVNDNSDKLTATYRKKEGVPVGSNPHTEFAARISKLGDVEI 259
QY 241 KFGNQAGSGSKDEKGNABIFITKGTQKLEITPTESNRIIAILDQNKSYTPGMEKA 300
DB 260 KFGNQAGSGSKDEKGNABIFITKGTQKLEITPTESNRIIAILDQNKSYTPGMEKA 319
QY 301 IMENKFTDSKAGNSDKYLGKAKSDNQAIMVSEKK 337
DB 320 IMENKFTDSKAGNSDKYLGKAKSDNQAIMVSEKK 356

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RESULT 2
Q9CKT8 PRELIMINARY; PRT; 348 AA.
AC Q9CKT8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PlpP.
GN Name=plpP; OrderedLocusNames=PM1518;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006188; AAK03601.1; -.
DR EMBL; AE006188; AAK03601.1; -.
KW Complete proteome.
SQ SEQUENCE 348 AA; 37362 MW; DCB2191499653P52 CRC64;

Query Match 15.6%; Score 270; DB 2; Length 348;
Best Local Similarity 25.8%; Pred. No. 1.5e-08;
Matches 97; Conservative 51; Mismatches 128; Indels 100; Gaps 17;

QY 1 CGGSGGSSSTPHKPVLPVKTQNNLQONVPOAQNAPQNAQNAQNAQNAQNAQV 60
Db 21 CGGGGGGSGNGNAPPV-----QPIQAPPAPHAQPPDA--APNI 58
QY 61 ENAPQNAQNAQ--VENAPQAEVTPVP-----QPQS--QKIDGSFDK---IGSVKLN 105
Db 59 P-APPKQCAPTGAKAPPAPAPAPANDSMGSPSAQKQWEGACEAKSVCAAKNEN 117
QY 106 KEAOTL-ELSEFTLVDK-LGTTPPKFKVSGKKIIEKDFLVNLSDINAEQLSGDFLIR 163
Db 118 KHVTVVYKLEHVENADRNSSTPDYKK-----EPEHITLNLGDSNGVEYKFTLLGSD 169
QY 164 SDDL-FYGYVHTNGKLVDAADKFSQYFVYDEKRVNDI-----SDKL 207
Db 170 GNEVGYGYRHN-----IDDSRAHKVVELLYAINTDFKSPDQSTQF 210
QY 208 TATYRKKEGFVYGSNPHTKFAARISKLGDEVEIKFENGQAQGSIKDKQKNA-----EI 261
Db 211 KAYYKKEGFYIAPISNTELSNGLINGVDNLYDNGSISGSIYSENGSETNKEEI 270
QY 262 FTI-KGDTKQLEIPTESNRIIILDONOKSYTPGMEKAIMETKFDISKAGNSDKYLI 320
Db 271 FKIEKGHSGSTIEP-----VLEHLLGTIKG-----DKANLNYILADSEKGNADHKYLF 320
QY 321 GEAKSDNQWQAIMVSEK 336
Db 321 GNAKAETWIGVLAEEK 336

RESULT 3
Q9CKT9 PRELIMINARY; PRT; 335 AA.
AC Q9CKT9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PlpP.
GN Name=plpP; OrderedLocusNames=PM1517;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.

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OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006188; AAK03601.1; -.
DR EMBL; AE006188; AAK03601.1; -.
KW Complete proteome.
SQ SEQUENCE 335 AA; 37449 MW; 5169813A26F7E7BB CRC64;

Query Match 12.8%; Score 221.5; DB 2; Length 335;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
Matches 79; Conservative 58; Mismatches 160; Indels 49; Gaps 10;

QY 2 GGGSGGSSSTPHKPVLPVKTQNNLQONVPOAQNAPQNAQNAQNAQNAQNAQV 61
Db 23 GGGGSAGNADRVEEK-----AQPV---QSNSEPSAPIKNPTNTATNDSLHD 67
QY 62 NAPAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 114
Db 68 KLSMSHSDTSKENSQQSSPKALEKQKQPAQENLTWGHVSEVGNASNNVVDKDNVTV- 126
QY 115 RPTLV---DKLGTTPPKFKVSGKKIIEKDFLVNLSDINAEQLSGDFLIRSDLFYGY 171
Db 127 -FTFVKYNSQYNDPFDKTKTQS-----KTISLVGKQNKEDYNYNFTLKDALF-- 175
QY 172 YHDTNGKLVDAADKFSQYFVYDEKRVNDIISDKLTATYRKKEGFVYGSNPHTKFAAR 231
Db 176 YGSGGQSPADYKVKYKNTYIAKPDANNENLNALTATYYQEDGFYISLVSDVNRVSGE 235
QY 232 -ISKLGDEVEIKFENGQAQGSIKDKDQNAEIFTIKGDTKQLEIPTESNRIIILDONQ 290
Db 236 YIPOYGVNVLTFERNKIYGEIVRYNRRGDDLQSLGEGQNLTITPHK-----DNPH 286
QY 291 KSYTGMKAMNETKFDISKAGNSDKYLIKEAKSDNQWQAIMVSEK 336
Db 287 KLSPTGPDNNAMELNFIN--AEKTDKYYVGVGKAERYIYGLLFAEK 330

RESULT 4
Q6JSM4 PRELIMINARY; PRT; 1158 AA.
AC Q6JSM4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-antigen.
GN Name=beta;
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98-D60C;
RA Dmitriev A., Shen A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (by similarity).
DR EMBL; AY598359; AAT10376.1; -.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR005877; Gpos_YSIrk.
DR InterPro; IPR001899; Gpos_pos_anchor.
DR InterPro; IPR003599; IG.
DR InterPro; IPR011047; Quin_alc_DH_like.
DR InterPro; IPR007756; RICH.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF05062; RICH_1.
DR Pfam; PF04650; YSIrk_signal; 1.
DR ProDom; PD153432; Csurface_antigen; 2.
DR SMART; SM00409; IG; 1.

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Qy	171	YHDTNGKGLVDAADKSQIFVVVD-----EKVNNDNISKLTYATRKKEGFVGSN	222
Dd	987	---HKTGGGT-----RVFDLSLKGSKETHVNGERTVRIALQGTSDDHVY---	1030
Qy	223	PHTKEFAARISKLGDNVE---IKFENGQAQSINKDEKDGNAEFTTKGDTKGLEITPTTESN	279
Dd	1031	HVKE-----NGDLERIPSKVENGQV-----PXTNHFSFLAIKTLSKDNQNVTPPKQT	1077
Qy	280	RIIAILDQNKSYTPGWKAIMEET---KFIDSKAGN	313
Dd	1078	-----KPSTQSQSVEIAESQTGRF-QSKAAN	1102
 RESULT 6 Q9CKU2			
ID	Q9CKU2	PRELIMINARY;	PRT; 331 AA.
AC	Q9CKU2;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-JAN-2004 (TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein PW1514.		
GN	Oredered locus names=PW1514;		
OS	Pasteurella multocida.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurillaceae; Pasteurella.		
OX	NCBI_Taxid=747;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Pm70;		
RX	MEDLINE=21145866; PubMed=11248100;		
RA	May B.J.; Zhang Q.; Li L.L.; Paustian M.L.; Whittam T.S.. Kapur V.;		
RT	"Complete genomic sequence of Pasteurella multocida Pm70.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).		
RD	ENBL; AB006188; AAK03598.1; --		
RR	Complete proteome; Hypothetical protein.		
SQ	SEQUENCE 331 AA; 37271 MW; 8CC9DA01EDC4EAA CRC64;		

Query Match	10.08;	Score 174;	DB 2;	Length 331;
Best Local Similarity	22.08;	Prod No. 0.0094;		
Matches	79;	Conservative	Mismatches 131;	Indels 76; Gaps 18;
Qy	1	CGSGSGSGSSSTPNH-----PKPVL--VPTQNNLQAO-----NVPQAQNASQAQN	44	
Db	21	CGSGGGGGNNNS-NHQAHFNVQPAFLHVAKPQOHVEQEVIEKKPVPVTRTASG--	77	
Qy	45	APQAQNAQAQNAQVQENNAQAQNAQVNAQAQVTPPVPQSQKTDGGSFDKIGSVKL	104	
Db	78	-----SFYSKAPQGVHDKRSVHWKGSVSSEKEHLDFSY-----	112	
Qy	105	NKEAQTLSEFTLLVDLXLGTPPKDFKUSGKKIIEBKD--FLVLNLSLDINAEQLSG-DPLI	161	
Db	113	SKDA-----VPTRLHVTNPNAVYSTDPNLI-SKDIKXITLITTTGTGNQDNKSGPNVEL	163	
Qy	162	RRSDD-LPYGYHHDTNGKLVDAADFQSYFVVYDEKRVNDNISDKLTATYRKKEGFVYG	220	
Db	164	NLLDENIYGYRDSQDMNHVE-----NLYVYGFKKDAEQNDNQLOFTANTYQGFLESTA	218	

Qy	221	SNPTKEPAARISKLGVEIKFENGQAQSIRKDEXDGNAEIFTIKGDTK--QLEBITTES	278
	:	: :::	:
	:	: :::	:
	:	: :::	:
Dd	219	TWPN-----VPVLGXVNLNXXEGRKAGELL-ERDSNVKLFDIYVNERPQAILNPV-A	269
	:	: :::	:
	:	: :::	:
	:	: :::	:
Qy	279	NRIIALLDQNKSYTFGMEKAMETKFIDSKAGNSDKOYLIGEAKNSNQAIINVSSEKK	337
	:	: :::	:
	:	: :::	:
	:	: :::	:
Dd	270	EELPTSLLIMTRKNSP--DRVTIDLHFIIKGQ-QRQENKYIVQGQNEKYGVGLGLEKK	325
	:	: :::	:
	:	: :::	:
	:	: :::	:
RESULT	7		
Q75WB4			
ID	Q75WB4	PRELIMINARY;	PRT; 1083 AA.
AC	Q75WB4;		
DT	05-JUL-2004	(TRENBLrel. 27, Created)	
DT	05-JUL-2004	(TRENBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TRENBLrel. 27, Last annotation update)	

```

DE C protein beta antigen.
GN Name=cba;
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FM027022;
RX MEDLINE=2112915; PubMed=12117978;
RA Nagano N., Nagano Y., Taguchi F.;
RT "High expression of a C protein beta antigen gene among invasive
RT strains from certain clonally related groups of type Ia and Ib group B
RT streptococci."
RL Infect. Immun. 70:4643-4649(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FM027022;
RA Nagano N., Nagano Y., Inoue M.;
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AB121739; BAC98831.1; -.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR011047; Quin_alc_DH_like.
DR InterPro; IPR007756; RICH.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF05062; RICH; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR SMART; SM00409; IG; 1.
DR TIGFAMS; TIGF01167; LPXTG_anchor; 1.
DR TIGFAMS; TIGF01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 1083 AA; 122150 MW; 83E08B5AC912FA78 CRC64;

Query Match 10.0%; Score 173; DB 2; Length 1083;
Best Local Similarity 23.7%; Pred. No. 0.045;
Matches 76; Conservative 45; Mismatches 110; Indels 90; Gaps 15;

QY 12 TPNHKPVLPVPTQNNLQAQNVPOQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
778 TPDTKIPELPQAPDTPQADTPHVPSPKAPAPRVPEPKTPEAHPVPEPKTPEAPK 837
QY 72 VENAPQAEVTPVPQ-----POSQKIDGSFDKIG-SVKLNKEAQTLELSRFTLVKLGTPP 126
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
838 IPEPKTDPVKLPDVKLPDAPKLPDGLNKVGQAVFTSDGNT-----KVTVV----- 886
QY 127 KFDKVGSKKIIIEKDFVLNLSDNAQLSGDFLIRSDDLFYGYHDTNGKNLVDAADK 186
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
887 -FDKPT-----DADKHLKEVTTKELADKIA-----HKTGGTV----- 919
QY 187 FSQYFVVVD-----EKRVDNISDKLTATYRKKEGFVYGSNPHTKFAARISKLGDV 238
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
920 -----RVFDLSLSKGGKETHVNGERTVRLALGQTGSDVHVY-----HVKE-----NGDL 963
QY 239 E---IKFENGQAQGSIKDEKGNAEIFTIKGDTKQLEITPTESNRRIIILDQNKSYTP 295
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
964 ERIPSKVENGQV-----FKTNHPSLFAITLSKDQNVTPPKQT-----KPSSTQ 1007
QY 296 GMEKAIMET---KFIDSKAGN 313
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1008 GSQVEIAESQTGKF-QSKAAN 1027

RESULT 9
Q99051 PRELIMINARY; PRT; 1134 AA.
AC Q99051;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fc receptor.
GN Name=bac;
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB35;
RX MEDLINE=91257158; PubMed=2044657;

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SEQUENCE FROM N.A., AND SEQUENCE OF 38-48.
STRAIN=LA239;
MEDLINE=91312121; PubMed=1857207;
Jelstroom P.G., Chhatwal G.S., Timmis K.N.;
"the IGA-binding beta antigen of the c protein complex of Group B
streptococci: sequence determination of its gene and detection of two
binding regions.";
Mol. Microbiol. 5:843-849(1991).
[2]
IDENTIFICATION OF IG-LIKE DOMAIN.
MEDLINE=97035265; PubMed=8880921;
Batsman A., Eddy S.R., Chothia C.;
"Members of the immunoglobulin superfamily in bacteria.";
Protein Sci. 5:1939-1942(1996).
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (Potential).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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or send an email to license@isb-sib.ch).
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EMBL; X59771; CAA42442.1; -
PIR; S15330; FCSOAG.
InterPro; IPR004829; Csurface_antigen.
InterPro; IPR005877; Gpos_YsIRK.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR007110; Ig-like.
InterPro; IPR007756; RICH.
InterPro; IPR010989; t-snare.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF05062; RICH; 1.
Pfam; PF04650; YsIRK_signal; 1.
ProDom; PD153432; Csurface_antigen; 1.
TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
TIGRFAMs; TIGR01168; YsIRK_signal; 1.
PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
PROSITE; PS00835; IG_LIKE; FALSE_NEG.
Cell wall; Direct protein sequencing; Immunoglobulin domain;
peptidoglycan-anchor; Receptor; Signal.
SIGNAL 1 37
CHAIN 38 1135 IGA FC receptor.
PROPER 1136 1164 Removed by sortase (Potential).
DOMAIN 434 534 Ig-like.
DOMAIN 199 438 IGA-binding (Potential).
DOMAIN 439 826 IGA-binding (Potential).
DOMAIN 827 944 Pro-rich.
DOMAIN 1132 1136 LPXTG sorting signal (Potential).
FT PT SITE pentaglycyl murein peptidoglycan amidated
FT FT MOD_RES threonine (Potential).
SEQUENCE 1164 AA; 131051 MW; 65DE94AF720A5474 CRC64;
Query Match 10.0%; Score 173; DB 1; Length 1164;

```

Qy	12	TPNHKPVLPKTONNLQAQNVFQAQNASQAQNAPOAQNAPQVENAPOAQNAPO 71
Db	829	TPPTPKTPELPQADPTQADTTHVPESPKAPEAPVPESPKTPEASHVPESPKAPEAPR 888
Qy	72	VENAPQAEVTPPVQ---PQSQKIDGSPFKISGVKLKEAQLTLESRFTLVDKLGP 127
Db	889	VPESPKTEAPHVPESPKTPEAPKIP-----EPKTPDVFKLPDVKLPDVPK 936
Qy	128	-----FDKVGSK---KTIEX--DFLVINTSDINAEQLSGDFLIRRS 164
Db	937	LPDAPKLPDGLNKVGQAVFTSTDGNTKVTVVFDKPTDADKHLKXEVTTKELADKXIA --- 992
Qy	165	DDLFPYGYHDNGKULVDADKFSQFWYD-----EKRVNDNISDKLTATYRKXEG 216

```
Db 993 -----HKTGGTV-----RVFDSLKSGKETHVNGERTVRLALGOTGSDV 1033
QY 217 FVYSGNPHKFAARISKLDGVE---IKPENGQAQGSINKDEKGNAEIFTIKGDFKQLEI 273
Db 1034 HVY-----HVKE-----NGDLERIPSKVNGQV-----FKTNHFSFAIKTISKQDNV 1077
QY 274 TPTESNRHIIAIDQNKXYTPGMEKAIMET---KFIDSKAGN 313
Db 1078 TPKQOT-----KPSQTQSGVETAEASQTGKF-QSKAAN 1108

RESULT 11
Q8TLE6 PRELIMINARY; PRT; 1443 AA.
AC Q8TLE6; MEDLINE=22092622; PubMed=12097910;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Similar to Mus musculus (Mouse). GABA-A receptor epsilon-like
DE subunit.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116960; AAM08494.2;
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 1443 AA; 167562 MW; 145B36EBF31D7350 CRC64;

Query Match 9.9%; Score 172; DB 2; Length 1443;
Best Local Similarity 25.0%; Pred. No. 0.074;
Matches 82; Conservative 48; Mismatches 130; Indels 68; Gaps 12;

QY 7 GGSSTPHNPKPVLVPTQNNLQNVPOQNASQAQNAPOQNAPOQNAPOQNAPOQNAPOQ 66
Db 362 GFSTQALUSQPTTAP-----ISFSAQSOPQ-QPQSQSQSQSQSQSQSQSQSQSQSQSQ 417
QY 67 QNAPQVNAPOQAEVTPVPQPSQKIDGSPFKIGSVKLNKEAQTLESLRFLVDKLGTPP 126
Db 418 QSQPTPSAPIGFSTQSQPQLOLQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 460
QY 127 KFDKVGKIIIEKDFVLNLSNADNAQSGDFLIRSDDLFGYHYHDTNGKNLVDAADK 186
Db 461 KFIST-----FSQGSFNNNNNNNNNDQFIELSRLSYDL-----ER 498
QY 187 FSQFVYVDEKRVNDISDKLTATYRKKEGVYSGNPHKFAARISKLDGVZIKENQ 246
Db 499 FKNVLL--ENKSNVDNIIKVN-NHKOMGEKLGNN---IDRCFENKFKVTSNISFNMD 552
QY 247 -----AQGSIKDEKGNAEIFTIKGDTKOLEITPTESNRHII-----AILDQNK 292
Db 553 FDLRIQNYFSTNQDEFNKNIEKTISSNTRLLNLLPSKWNQLLPDFTNFCLDPDGT 612
QY 293 YTPGMEKAIMETKIDSKAGNSDKYLI 320
Db 613 YF-----SIDKKETIDWIFENLKNQYFI 635

RESULT 12
Q8BMN8 PRELIMINARY; PRT; 405 AA.
AC Q8BMN8; MEDLINE=99279253; PubMed=10349636;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:5330409A03 product:weakly similar to GLUTAMINE
DE REPEAT PROTEIN-1.
GN Name=L3mbtl3; (Mouse).
OS Mus musculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
```


DR EMBL; AK129443; BAC98253.1; --
 FT NON TER 1
 SQ SEQUENCE 761 AA; 85935 MW; A21FF7411767346C CRC64;
 Query Match 9.3%; Score 162; DB 2; Length 761;
 Best Local Similarity 52.7%; Pred. No. 0.14; Mismatches 26; Indels 6; Gaps 2;
 Matches 39; Conservative
 QY 21 VKPTQNNLQAQNV---QAQNASQAQNAPOAQAQNAPOV---ENAPQAQNAPOVEN 74
 Db 556 VQHAQPPQAQAPQAQQAQQAQQAQAPQTPQPPQAQVQAQQAQQAQQAQPPQ 615
 QY 75 APQAEVTPPVQPQ 88
 Db 616 AQQPQAQPPVQPQ 629
 RESULT 16
 Q8BLB7 PRELIMINARY; PRT; 883 AA.
 AC Q8BLB7;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Mus musculus adult male corpora quadrigenina cDNA, RIKEN full-length
 DE enriched library, clone:B230219004 product:weakly similar to GLUTAMINE
 DE REPEAT PROTEIN-1.
 GN Name=L3mbtl3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA The FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtration of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kanno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hata A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK045667; BAC32449.1; --
 DR HSP; P39769; 1KW4.
 DR MGD; MGI:2143628; L3mbtl3.
 DR InterPro; IPR000886; ER target_S.
 DR InterPro; IPR004092; Mbt.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF02820; Mbt; 3.
 DR Pfam; PF00536; SAM 1; 1.
 DR SMART; SM00561; Mbt; 3.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00014; ER TARGET; UNKNOWN_1.
 DR PROSITE; PS0105; SAM DOMAIN; 1.
 SQ SEQUENCE 883 AA; 99137 MW; 7A6417202A0E5532 CRC64;

Query Match 9.3%; Score 162; DB 2; Length 883;
 Best Local Similarity 52.7%; Pred. No. 0.17;
 Matches 39; Conservative 3; Mismatches 26; Indels 6; Gaps 2;

QY 21 VKPTQNNLQAQNV---QAQNASQAQNAPOAQAQNAPOV---ENAPQAQNAPOVEN 74
 Db 678 VQHAQPPQAQAPQAQQAQQAQQAQAPQTPQPPQAQVQAQQAQQAQQAQPPQ 737

QY 75 APQAEVTPPVQPQ 88

Db 738 AQQPQAQPPVQPQ 751

RESULT 17

Q9RCG1

ID Q9RCG1 PRELIMINARY; PRT; 365 AA.

AC Q9RCG1;

DT 01-MAY-2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)

DE Outer membrane lipoprotein.

OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Actinobacillus.

OX NCBI_TaxID=715;

[1]
 RP SEQUENCE FROM N.A.

RC STRAIN=8329;

RX MEDLINE=98126231; PubMed=9466755;

RA Gram T., Ahrens P.;

RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae
 RT based on the nucleotide sequence of an outer membrane lipoprotein.";

RL J. Clin. Microbiol. 36:443-448(1998).

DR EMBL; U86687; AAD00620.1; --

DR InterPro; IPR005014; Lipoprotein_14.

DR Pfam; PF03346; Lipoprotein_14; 1.

KW Lipoprotein.

SQ SEQUENCE 365 AA; 39750 MW; E20A60DB246DAES CRC64;

Query Match 9.3%; Score 160.5; DB 2; Length 365;

FT	CHAIN	20	365	Outer membrane lipoprotein A.
FT	LIPID	20	20	N-palmitoyl cysteine (Probable).
FT	LIPID	20	20	S-diacetylglycerol cysteine (Probable).
SEQ	SEQUENCE	365 AA;	39784 MW;	200453FAEBE2842F CRG64;

Query Match	9:2%;	Score 159.5;	DB 1;	Length 365;
Best Local Similarity	24.1%;	Pred. No. 0.081;		
Matches	92;	Conservative	54;	Mismatches 139;
				Indels 97;
				Gaps 21;

QY	1	CGSGSGSGSSSTNHPKPVLPVKTQNNLOAQNVPOQAQNASQAQVAPQAQNAQAQN----	56
DB	20	CSGGSGSGSSSKPNS-----LTPKVD-----MSAPKAEQ-----PKGEVPOADSKAE	64
QY	57	-----APOVENAPQAQN-----APOVENA-----PQAEVTPVPVPOQSQKIDGSPDKIGSVK	103
DB	65	EPKEMAPQVD-SPKAESEPKMAPQGNPKLNDPQV-MAFKMNPQKDAKPG-----E	115
QY	104	LNKEAQTLELSRFTLVDKL--GTPPKFDKVGSKKIIEEKDFL-----VLNLSLDINAEQLSGDF	159
DB	116	LSKDKSNAEILKELGVKDINSGLINNADVVLNLK-IDEKDHIITVLDKGINENHLKVTN	174
QY	160	LIRSDDLFGYYHYDNGKNLVDAADKFSQY-----FVYVDEKRVNDNTSDKLTAIVRKKEGF	217
DB	175	TISAQDI-----KTLKDSGKLLGYGYMWQLNQVRQDENYSDEKVSF-----NEYV	220
QY	218	YVGSNPHTKFAAR-ISKLGDVETKE-----NGQAQSGIKDEKQGNAEIFTK-----	265
DB	221	LLSMNDADKIRP*KSISYKGMFYSKDVGKNQKLKASVEASDYDVTCKVSMKVFGENDY	280
QY	266	-----GDTKQLEITTES-----NRIITAILDQNKSYTPGMEKAIMETKFDISK	310

QY	311	AGNSDQKYLIGEAQSDNQWAIM	332
	:	: : : :	:
DB	334	FGXNGE-VLAGSAISEKWQGV	354
RESULT 19			
Q9R3L8		PRELIMINARY;	PRT; 365 AA.
ID	Q9R3L8		
AC	Q9R3L8;	2000 (TREMblrel_13, Created)	
DT	01-MAY-2000	(TREMblrel_13, Last sequence update)	
DT	01-MAY-2000	(TREMblrel_13, Last sequence update)	
DE	05-JUL-2004	(TREMblrel_27, Last annotation update)	
DE	Outer membrane lipoprotein.		
OS	Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurellaceae; Actinobacillus.		
OX	NCBI_TaxID=715;		
RN	[1]		
FN	SEQUENCE FROM N.A.		
RP	STRAIN=56153, S4074, and CVI 13261;		
RC	MEDLINE=98126231; PubMed=9466755;		
EX	Gram T., Athens P.;		
RA	"Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae based on the nucleotide sequence of an outer membrane lipoprotein.";		
RT	J. Clin. Microbiol. 36:443-448(1998).		
RL	EMBL; U86686; AAD00619.1; -		
DR	EMBL; U86675; AAD00608.1; -		
DR	EMBL; U86684; AAD00617.1; -		
DR	InterPro; IPR005014; Lipoprotein_14.		
DR	Pfam; PF03346; Lipoprotein_14; 1.		
KW	Lipoprotein.		
SQ	SEQUENCE 365 AA; 39842 MW; 5B46DFCBB542781E CRC64;		
Query Match 9.2%; Score 159.5; DB 2; Length 365;			
Best Local Similarity 24.1%; Pred.No.0.081;			
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21			
QY	1	CGSGSGGSSSTPNHXPVLVPKTTNNILQAQNVPQAQNASQAQAPQAQNAPOAQN	--- 56
	:	: : : :	:
DB	20	CSGGSGGSSSKPNSKSE-----LTTPKYD-----MSAPKAQE-----PKKEEYPQADNSKAE	64

Query Match	9.2%	Score 159.5;	DB 2;	Length 365;
Best Local Similarity	24.1%;	Pred. No. 0.081;		
Matches 92;	Conservative 54;	Mismatches 139;	Indels 97;	Gaps 21
QY	1	CGGGSGGSGSTPHHPKLVLPKTNMLQAVTSCAQWASQAQWAPQANAPQANQ	----	56
DB	20	CSGGSGGSGSKPSE---LTPKVD-----MSAPKAEQ-----PKKEEVPQADNSKAE	64	

QY 57 -----APOVENAPQAN-----APOVENA-----POAEVTPVPQSQKIDGSPDKIGSVK 103
DB 65 EPKEMAPQVD-SPKAEPPKNAPOGNPKLNDPQV-MAPKMDNPCKDAPKGE-----E 115
QY 104 LNKEAQTLESLFTLVKLI--GTPPKFDKVSCKKIIIEKDEL--VLNLSDNAQLSGDF 159
DB 116 LSKDKSNAELKELGVKDINSIINNADVVLNLK-IDEKDHITVVLDKDKINRHLKVTN 174
QY 160 LIRSDDLFYGYHDTNGKLVDAADKFSQY--FVYDEKRVNDNISDKLTATYRKKEGF 217
DB 175 TISAQDI-----KTLKSSGKLLGYGVYQVQLNQVRQDENYSDEKVSLL--NEY 220
QY 218 VYGSNPHKFAAR-ISKLGDEVEIFE--NGQAGSINKDEKGNABEFTIK----- 265
DB 221 LLSMDADKIRPTKISYKGMFYSYKDVGNQKLKASVEASVDDVTKKVSMKVFGENNDY 280
QY 265 -----GDTKOLEITPTES-----NRIIALDQNKSYTPGMEKAIMETKFDISK 310
DB 281 WKLGEGFRINLLENQVTGAKVGEDGTIINGLYSKIDNFKLTP-----DANFSGGI 333
QY 311 AGNSDKVILGSAKSDNQAIM 332
DB 334 FGKNGE-VLAGSAISEKQWGI 354

RESULT 20

P91448 PRELIMINARY; PRT; 896 AA.
AC P91448;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-2000 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Prion-like (O/N-rich)-domain-bearing protein protein 66.
GN Name=pqn-66; ORFName=T16A1.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodexinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Goela D.;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.,"
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U0454; AA037876.3; -;
DR WormPep; T16A1.7; CE32724.
KW Prion.
SQ SEQUENCE 896 AA; 101378 MW; 3A91076B7E346837 CRC64;

Query Match 9.2%; Score 159.5; DB 2; Length 896;
Best Local Similarity 33.1%; Pred. No. 0.24;
Matches 50; Conservative 21; Mismatches 57; Indels 23; Gaps 7;

QY 3 GSGSGSSSTPNHPKVLVPTQNNLQAQNVPOAQNASQAQNAPO---AQNAPQAQNAPO 59
DB 732 GQNAFDQNAQNDNAQNAFNVQNSQNTNAQNSQNAQNAFNAQIAQNDNAPNAQI 791
QY 60 VENAPOAQ---NAPQVEN---APOAEVTPVPQSQKIDGSPDKIGSVKLNKEAQTLEL 113
DB 792 AQNAFNAQNDINAFNVQNAQNAPOAQNAQQAQQAQKELE---KEIGQFLCKRSFGVLE- 847

QY 114 SRFTLVKLTGTPPKFDK-----VSGKKIIEK 140
DB 848 ---GLMDLVG---GFPEKHTLDVSTLTKIKEK 872
RESULT 21
Q9RCG2 PRELIMINARY; PRT; 375 AA.
AC Q9RCG2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Outer membrane lipoprotein.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M62;
RX MEDLINE=98126231; PubMed=9466755;
RA Gram T., Ahrens P.;
RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae
based on the nucleotide sequence of an outer membrane lipoprotein.,"
RL J. Clin. Microbiol. 36:443-448(1998).
DR EMBL; U86678; AAD00611.1; -;
DR InterPro; IPR005014; Lipoprotein_14.
DR Pfam; PF03346; Lipoprotein_14; 1.
KW Lipoprotein.
SQ SEQUENCE 375 AA; 40840 MW; 67BA62BES8E01A02 CRC64;

Query Match 8.9%; Score 155; DB 2; Length 375;
Best Local Similarity 24.1%; Pred. No. 0.16;
Matches 98; Conservative 47; Mismatches 126; Indels 136; Gaps 26;
QY 1 CGSGSGSSSTPNHPKVLVPTQNNLQAQNVPOAQNASQAQNAPOAQNAPOV 60
DB 20 CGSGSGSSSSSKFN-SKP--TPKVDMSAPKAEQPKKEVPQAEQ-PKKEEVPQA-DSPKA 74
QY 61 EN-----APOAQAPOVENAPQAEVTPVPQSQKIDGSPDKIGSVKLNKEAQTLELSP 116
DB 75 EKPKSIAPLMENPKVEXQENNL-----QEKSPRAD-----EFQVMD----- 112
QY 117 TLVVDKLTGTPPKFDK-----VSGKKIIEE---KDF-----LVNLSDINAE----- 153
DB 113 ---PKLGAPQKDDQKLEPKNKSNAILKELGKIDKTIITRSDVNLNLTIDQENIQI 169
QY 154 QLSGDFLIR-----SDDL-----FYGYH-----DTNGKNLVDAAD 185
DB 170 RLSESDIVRNDLKITNTPNQDITRLKDSGTGLGYGYGMQLNQVREGERYGINNVDLV- 228
QY 186 KFSQYFVVYVDEKRVNDNISDKLTATYRKKEGVYG-SNPHTKEFAARISKLGDEVEIKEN 244
DB 229 ---GHYLLSMD---STKTA PKSIERYGK--MLYKKNVDNRNLVA-----DVQASNH 275
QY 245 GOAQGSIKDEKGNABEFTIKGDTKQL-----EITPTESNRIIAIL 286
DB 276 -----SDKKLSMEIFGDHGYWKLGAIGNNRLPKDMVTGVVVVDKGTISNAGLYSKI 327
QY 287 DQNKSYTPGMEKAIMETKFDISKAG-NSDQKYLIGEAQSDNQAIM 332
DB 328 DN-----TFG--KLTPDATFGGIFGKNGD--VLAGSADGKNQWGI 365

RESULT 22

O15687 PRELIMINARY; PRT; 194 AA.
AC O15687;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Merozoite surface protein 2 (fragment).

QY	111	LELSRFTLVKDLGTPPKFVSKGKIIIEKDFLV-LNLGSDINAEQLSGDPLIERSDDL--	167
Db	132	KDI:::KGIITRSDVNLNLTIDENIQIRLSESDIVENDLKITWTIPNQDIRTL	184
QY	168	---FYGYH:---DTNGKLVDAADKFSQYFVVVYDEKRVNDSISDKLTATY	211
Db	185	KDSTGRLLGYGYMQLNVQVREGERYGINNVDLV---CHVLLSMDE---STKTAPNKSIEY	238
QY	212	RKEGFFVG-SNPHTKEFAARISKLGVEIKFENGQAQGSIKDEKDGNAEIFTIKGDTKQ	270
Db	239	RGK--MLYGYKYNDRNLVA---DVOQSYNH---SDKLSMEIFGDHGDYWK	282
QY	271	L---EITPTESNRITIIALDONQKSYTSGMEKAIMETKFDISKAG	312
Db	283	LGAIGNRLPKDMVTGVVDDKGTISNAGLYSKIDN---TFG--KLTPDATFSGGIFG	335
QY	313	NSDQKYLIGAEKSDNWQAIM	332
Db	336	KNGD--VLAGSADGKNWQGI	354

RESULT 24

Q9RCG3

PRELIMINARY;

PRT;

368 AA.

Q9RCG3

AC

Q9RCG3;

01-MAY-2000 (TrEMBLrel. 13, Created)

DT

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT

01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE

Outer membrane lipoprotein.

OS

Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).

OC

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC

Pasteurellaceae; Actinobacillus.

NCBI_TaxID=715;

RN

[1]

SEQUENCE FROM N.A.

RP

STRAIN=S1536;

RC

MEDLINE=98126231; PubMed=9466755;

RX

Gram T., Ahrens P.;

RA

"Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae

RT

based on the nucleotide sequence of an outer membrane lipoprotein."

RT

J Clin. Microbiol. 36:443-448(1998).

EL

EMBL; U86676; RAD00609.1; --

DR

InterPro; IPR005014; Lipoprotein_14.

DR

Pfam; PF03346; Lipoprotein_14; 1.

DR

Lipoprotein.

KW

LIPOPROTEIN

QY

SEQUENCE

368 AA;

39967 MW;

0281948BFB2B8E783

CRC64;

Query Match

Best Local Similarity

Matches

93;

Conservative

8.5%;

Score 147;

DB 2;

Length 368;

24.2%;

Pred. No. 0.47;

139;

Indels 100;

Gaps 24;

QY	1	CGSGSGSGSSSTPNHPKFLVLPVPTQNNLQCNVPAQNASQAQNAPOAQN----	56
Db	20	CSGSGSGSSSKNSE--LTPKVD-----MSAPKAEQ-----PKKEEVPQADNSKAE	64
QY	57	-----APQVENAQAQN-----APQVENA-----PQAEVTPVPQSQKIDGSPKIGSVK	103
Db	65	EPEKMAPOVD--SPKAEFPQMAPQMGPKLNDPOV--NAPKVDNPQKDPAPGE-----E	115
QY	104	LNKEAQTLLEISRFLVDKL--GTPPKPKYSGKKIIEKD--FVLNLSDINAEQLSGDF	159
Db	116	LSKDKSNAEILKELGVZDINGSIINNADVNLNK-IDEKQIKIVLQKSEINRSLKVTN	174
QY	160	LIRASDDL-----FYGY-----HDINGKNLVDAADKFSQYFVVYDEKR	198
Db	175	AIPTQDIKTLKSSGKLLGYGYMQLSQVRQDESYSTDSLNL-----SNYYLLSMNEQ	227
QY	199	VNDNISDKLTATYRKKEGFFVG--SNPHTKEFAARISKLGVEIKFENGQAQGSIKD----	253
Db	228	EKTRPSKSLT-----YKGTMIYGVSSVANNKLEAEVKAQYDHSSKKLSMQVFGQNEHWRL	283
QY	254	-EKDGNAEIFTIKGDTKQL-EITPTESNRI--IIAILDQNKSYTPGMEKAIMETKFDIS	309

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DB 284 ABASG---INNVLKPSKLRDVIIVSDKGDINGLLYLEDSTPSKFTTP-----NANFSGG 333
QY 310 KAGNSDQKYLIGEAKS--DNWQAIM 332
DB 334 FFGKNGE-VLAGKAESIKGEWQGV 357

RESULT 25
Q9RIH8 PRELIMINARY; PRT; 368 AA.
AC Q9RIH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane lipoprotein.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=405;
RX MEDLINE=98126231; PubMed=9466755;
RA Gram T., Ahrens P.;
RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae
RT based on the nucleotide sequence of an outer membrane lipoprotein.";
RL J. Clin. Microbiol. 36:443-448 (1998).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=405;
RX Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.
RA EMBL, U86683; AA00616.2;
DR InterPro; IPR005014; Lipoprotein_14.
DR Pfam; PF03346; Lipoprotein_14; 1.
KW Lipoprotein.
SQ SEQUENCE 368 AA; 40031 MW; 9584C0ED96E6CC9A CRC64;

Query Match 8.5%; Score 147; DB 2; Length 368;
Best Local Similarity 24.2%; Pred. No. 0.47;
Matches 93; Conservative 53; Mismatches 139; Indels 100; Gaps 24;

QY 1 CGSGSGSSSTPHPKFVLVPTQNNLQAVPQNAQNASQAQAPQAPQAPQAN---- 56
DB 20 CSGSGSGSSSKPNSE---LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64
QY 57 -----APOVENAPQAN-----APQVENA-----PQAEVTPVPQSQKIDGSPKIGSVK 103
DB 65 EPKEVAPQVD-SPKAEPEKNAPQGNPKLNDPQV-MAPKMDNPKDAPKGE-----E 115
QY 104 LNKEAQTELEGRFTLVLDKL--GTEPKPKVSGKIIIEKD--FLVLNLSDINABQLSGDF 159
DB 116 LSKDKSNAELKELGVKGDINGSLINNADVNLK-IDKQIKIVLDKSEINRDSLKVTN 174
QY 160 LIRRDLL-----FVGYY-----HDNKGKMLVDAADKPSQYFVVYDEKR 198
DB 175 AIPTODIKTLKDSGKLLGYGYQMQLSQVRQDESYSYDLSNL-----SNVYLLSMNEQ 227
QY 199 VNDNLISDLKLTATYRKKEGFVVG-SNPHTKEFAARISKLGDVEIKFENGQAQGSIKD---- 253
DB 228 EKTRPSKSLT-----YKGTMIYGVSVANKEAEVKAQYDHSKSKLSNQVFGQDNHWRL 293
QY 254 -EKGNASIFIKGTGKQL-EITPESNRI--IIAILDQNKQSYTPGKXAIMETKFDIS 309
DB 284 ABASG---INNVLKPSKLRDVIIVSDKGDINGLLYLEDSTPSKFTTP-----NANFSGG 333
QY 310 KAGNSDQKYLIGEAKS--DNWQAIM 332
DB 334 FFGKNGE-VLAGKAESIKGEWQGV 357

RESULT 26
Q9VYV7 PRELIMINARY; PRT; 837 AA.
AC Q9VYV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CGI745-PB.
GN CRFNames=CGI745;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abrial J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.N., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.X., Wasserman D.A., Weinstock G.M., Weissbach J., Ye J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=2426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=2426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
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RT "Molecular profiles of group B streptococcal surface protein antigen
RL genes; relationship to molecular serotypes.";
RL J. Clin. Microbiol. 40:620-626(2002).
DR EMBL; AF362697; AAL56260.1; -.
DR InterPro; IPR004829; CSurface_antigen.
DR DR InterPro; IPR007756; RICH.
DR Pfam; PF05062; RICH. 1.
DR ProDom; PD153432; CSurface_antigen; 3.
FT NON_TER 1
FT 213 213
SQ SEQUENCE 213 AA; 22887 MW; 89E6CB7EBB0DA588 CRC64;

Query Match      8.3%; Score 143.5; DB 2; Length 213;
Best Local Similarity 24.7%; Pred. No. 0.39;
Matches 41; Conservative 35; Mismatches 69; Indels 21; Gaps 4

Qy 12 TPNHPKVLVPTQNTTLCQAQNVPQAQNASQAQNAPOAQAQAPQVENAPQAQNAPO 71
Db 48 TDTEPKIELPQAEDTPQAADPTHVPSPKAPKAPRVPSPKAPEAPRVPSFKTPEAPH 107
Qy 72 VENAPQAQEVPPVQPQ----POSQXIDGSFDKIGSVKLNKEAQLELSRRTLVDKLGTPPK 127
Db 108 VPESPKAPEARVPESPSTPEAPHVPSPKTPEAPKIPEPKTFDPVKLPDVPKLPDAPK 167
Qy 128 -----FKVSGK---KIIIEK--DFLVNLSDINAEQLS 156
Db 168 LPDGGLNKVGQAVFTTDGNTKVTVVFDPKPTDADKLHLKEVTTKELA 213

RESULT 28
Q9R3V2 PRELIMINARY; PRT; 365 AA.
AC Q9R3V2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Outer membrane lipoprotein precursor.
GN Name=omLA;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxId=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wf83;
RX MEDLINE=96376964; PubMed=8782813;
RA Chevallier B.;
RL "Palindromic structure of the lgh3' locus control region." ;
RT Nat. Genet. 14:15-16(1996).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wf83;
RX MEDLINE=99026959; PubMed=9809431;
RA Ito H., Osaki M., Uchida I., Ohya T., Sekizaki T.;
RT "Demonstration of the third antigenically distinct outer membrane
RL lipoprotein (OmLA) in Actinobacillus pleuropneumoniae serotype 7.";
RFEMS Microbiol. Lett. 167:303-308(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wf83;
RX MEDLINE=98126231; PubMed=9466755;
RA Gram I., Ahrens P.;
RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae
RL based on the nucleotide sequence of an outer membrane lipoprotein.";
RJ. Clin. Microbiol. 36:443-448(1998).
DR ENBL; AB007579; BA343662.1; -.
DR ENBL; U86682; AADO0615.1; -.
DR InterPro; IPR005014; Lipoprotein_14.
DR Pfam; PF03346; Lipoprotein_14; 1.
KW Lipoprotein; Signal.
FT SIGNAL 1
FT 19
SQ SEQUENCE 365 AA; 39708 MW; 3DFA543CC115C5F3 CRC64;
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QY      67 QNAPOVENAPQAEVTPVPQ-----PQSQKIDGSFDKIGSVKLNKEAQTLELSRFTLVDKL 121
DB      104 PDTTHVPESPKAPEAPRVPSPKTPEAPHVPESPKTPEAPKIPPEPKTDDVPKLPDVPKLP 163
QY      123 GTPPK-----FDKVSQK--KIIEEK--DFLVNLISDINAEQLS 156
DB      164 PDAPKLPDGLNKVGCAVFTSDGNTKTVVVFDKPTDADKLHLKEVTTKELA 214

ID Q7X579 PRELIMINARY; PRT; 249 AA.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C protein immunoglobulin-a-binding beta antigen (Fragment).
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K105-A4493/93;
RA MEDLINE=21630313; PubMed=11756648;
RX Berner R., Ruess M., Bereswill S., Brandis M.;
RT "polymorphisms in the cell wall-spanning domain of the C protein beta-
RT antigen in clinical Streptococcus agalactiae isolates are caused by
RT genetic instability of repeating DNA sequences.";
RL Pediatr. Res. 51:106-111(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K105-A4493/93;
RA von Both U., Berner R.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AY260003; AAP43681.1; -.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR007756; RICH.
DR Pfam; PF05062; RICH; 1.
DR ProDom; PD153432; Csurface_antigen; 3.
FT NON_TER 1
FT NON_TER 249 249
SQ SEQUENCE 249 AA; 26845 MW; C2D547E3C1F7C4C8 CRC64;

Query Match 8.0%; Score 139; DB 2; Length 249;
Best Local Similarity 28.6%; Pred. No. 0.89;
Matches 36; Conservative 22; Mismatches 58; Indels 10; Gaps 1;

QY      12 TPNHKPVLPKTKQNNLOAQNVFOAQNAQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQ 71
DB      55 TPDTPKIPETLPQAPDTPQAPDTPVPESPKAPEAPRVPSPKAPEAPRVPSPKAPEAPR 114
QY      72 VENAPOAEVTPVPQ-----PQSQKIDGSFDKIGSVKLNKEAQTLELSRFTLVDK 121
DB      115 VPESPKAPEAPRVPSPKTPEAPHVPESPKAPEAPRVPSPKTPEAPHVPESPKTPEAPK 174

QY      122 LGTPPK 127
DB      175 IPEPPK 180

RESULT 35
Q7X578 PRELIMINARY; PRT; 255 AA.
ID Q7X578
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C protein immunoglobulin-a-binding beta antigen (Fragment).
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=1311;

```

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=M13/99-22020;
RX MEDLINE=21630313; PubMed=11756648;
RA Berner R., Ruess M., Bereswill S., Brandis M.;
RT "Polymorphisms in the cell wall-spanning domain of the C protein beta-
RT antigen in clinical Streptococcus agalactiae isolates are caused by
RT genetic instability of repeating DNA sequences.";
RL Pediatr. Res. 51:106-111(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M13/99-22020;
RA von Both U., Berner R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY260004; AAP43682.1; -;
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR007756; RICH.
DR Pfam; PF05062; RICH; 1.
DR ProDom; PD153432; Csurface_antigen; 3.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27495 MW; E29B5440C141970A CRC64;

Query Match 8.0%; Score 139; DB 2; Length 255;
Best Local Similarity 28.6%; Pred. No. 0.92; Mismatches 10; Gaps 1;
Matches 36; Conservative 22; Indels 58; Indels 10; Gaps 1;

QY 12 TPNHPKVLVPTKQNNLQAVPQANASQANAPQANAPQANAPQANAPQANAPQANAPQ 71
DB 55 TPDTKIPQLPQAPDTPQADTPHVPSPKAPAPVPSPKAPAPVPSPKAPAPVPSPK 114
QY 72 VENAPQAEVTPVQ-----PQSKIDGSPKIGSVKLKNAQTLELRLFLVVK 121
DB 115 VPSPKAPAPVPSPKTPPEAPHVPSPKAPAPVPSPKTPPEAPHVPSPKTPPEAPK 174
QY 122 LGTPPK 127
DB 175 IPEPK 180

RESULT 36
Q6CCL1 PRELIMINARY; PRT; 1309 AA.
AC Q6CCL1
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P08640|Saccharomyces cerevisiae YIR019c|STAL
DE extracellular alpha-1.
GN ORFNames=YALI0C08473g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA LaFontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boirame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenn S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Selleniz D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts."

RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382129; CAG81904.1; -;
DR SEQUENCE 1309 AA; 137079 MW; 7D2E2927115D6CC2 CRC64;

Query Match 8.0%; Score 139; DB 2; Length 1309;
Best Local Similarity 28.2%; Pred. No. 6.6; Mismatches 38; Indels 14; Gaps 3;
Matches 29; Conservative 22; Indels 14; Gaps 3;

QY 9 SSSPTNHPKVLVPTKQNNLQAVPQANASQANAPQANAPQANAPQANAPQANAPQAN 68
DB 393 SSSPTSSAPV----TSSEFPSSIPETSSAPETSSAPETSSAPETSSAPETSS 448
QY 69 APOVENAPQA-----EVTTPVPOQSQKIDGSPDKIGS 101
DB 449 APETSSAPETSSERPSSSTPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 491

RESULT 37
Q7X584 PRELIMINARY; PRT; 201 AA.
AC Q7X584
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
DE C protein immunoglobulin-a-binding beta antigen (Fragment).
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M22/99-22019;
RX MEDLINE=21630313; PubMed=11756648;
RA Berner R., Ruess M., Bereswill S., Brandis M.;
RT "Polymorphisms in the cell wall-spanning domain of the C protein beta-
RT antigen in clinical Streptococcus agalactiae isolates are caused by
RT genetic instability of repeating DNA sequences.";
RL Pediatr. Res. 51:106-111(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M22/99-22019;
RA von Both U., Berner R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY259998; AAP43676.1; -;
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR007756; RICH.
DR Pfam; PF05062; RICH; 1.
DR ProDom; PD153432; Csurface_antigen; 2.
FT NON_TER 1
FT NON_TER 201
SQ SEQUENCE 201 AA; 21796 MW; 7F0F43EF959BAE96 CRC64;

Query Match 8.0%; Score 138.5; DB 2; Length 201;
Best Local Similarity 23.9%; Pred. No. 0.74; Mismatches 29; Gaps 4;
Matches 37; Conservative 30; Mismatches 29; Gaps 4;

QY 12 TPNHPKVLVPTKQNNLQAVPQANASQANAPQANAPQANAPQANAPQANAPQANAPQ 71
DB 55 TPDTKIPQLPQAPDTPQADTPHVPSPKAPAPVPSPKAPAPVPSPKAPAPVPSPK 114
QY 72 VENAPQAEVTPVQ-----PQSKIDGSPKIGSVKLKNAQTLELS 114
DB 115 VPSPKTPPEAPKIPPEPKTPDVVKLPDVKLPDVKLPDVKLPDVKLPDVKLPDVK 170
QY 115 RFTLVKLGTPPKFKVSGKKIIEKDFLVNLSD 149
DB 171 KVTVV-----FDKPTDADKLKLVKTTKELAD 197

OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13039;
RX MEDLINE=98126231; PubMed=9466755;
RA Gram T., Akrens P.;
RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae
based on the nucleotide sequence of an outer membrane lipoprotein.";
RL J. Clin. Microbiol. 36:443-448(1998).
DR EMBL; U86685; AAD00618.1;
DR InterPro; IPR005014; Lipoprotein_14.
DR Pfam; PF03346; Lipoprotein_14; 1.
KW Lipoprotein.
SQ SEQUENCE 367 AA; 40186 MW; 553653BEA98BDBA3 CRC64;

Query Match 8.0%; Score 138.5; DB 2; Length 367;
Best Local Similarity 22.1%; Pred. No. 1.5;
Matches 91; Conservative 61; Mismatches 105; Indels 155; Gaps 26;

QY 1 CGGSGGSSSTNHPKFLVLPKTONLQANVPOAQNASQAQNAPOAQN----APQAQN 56
Db 20 CSGGSGGSSPKPNSRS---TPKVDMSAPKAEPKKEEAPQA--DSPKAEPKSIAPLMWE 75

QY 57 APOVENAQAQNAQVENAPQA---EVTTP---VPOFQSQKIDGSFDK----- 98
Db 76 NPKVEK--QKENLIQ-EKSPKADEPQWMDPKLGAPQKDDQKLEEPKNKSNAEILKELGIK 132

QY 99 -----IGSVKLNKEAQTLELSRFTLV-----DKLGTTPKFDKVSQKIIEEKD--- 141
Db 133 DITSGTISIDIELNLQLDSNDNVKISLLNENLMRDNLTN---NKIAGSDIRTLKDSGG 189

QY 142 -----FLVLN-----LSDINAEQLSGDFLIRRSDDLFGYYH 173
Db 190 RLLGYGVQVQINQVTDQSRDPDNYKQFENHYLLSMNDAEKILPEKSLVKSGSMIYG-- 247

QY 174 DTRGNLVDAAKFSQYFVYVYDEKRVNDNISDKLTATYRKKEGFTVYGSNPHYKEFAARIS 233
Db 248 NTSG-----NEKLTAEVNAK-----YDSS--TKLSMKVY 275

QY 234 -----KLGDV---EIKFENGQAQSGTKDEKDG--NAEIFTIKGDTKQLEITPTESNRII 282
Db 276 DNDRYWKLGEVMSNNVLPPEEKVDG-VKVDSDGTINARLYL--STEEPLKLT----- 325

QY 283 IAILDQNKSYTPGMEKALMETKFIIDSKAGNSDQKYLIGEAKS--DNWQAIM 332
Db 326 ----DAN---FSGG-----IFGKNG-----EVLAKAESIKGEWQGI 356

Search completed: December 17, 2004, 16:01:41
Job time : 225.711 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 15:52:32 ; Search time 44.3421 Seconds
(without alignments)
731.247 Million cell updates/sec

Title: US-10-696-544-2
Perfect score: 1734
Sequence: 1 CGSGSGSGSSFPNHPKPV.....YLIGBAKSDNQAIWVSEKK 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	10.2	1164	1 FCSOAG	IgA Fc receptor pr
2	173	10.0	1134	2 A60234	IgA Fc receptor pr
3	159.5	9.2	365	2 A49235	outer membrane lip
4	159.5	9.2	456	2 C88065	protein T16A1.6 [i
5	141	8.1	3164	1 WMSR6	UL36 protein - hum
6	138.5	8.0	367	2 I39649	lipoprotein - Acti
7	135.5	7.8	785	2 H90547	lipoprotein [impor
8	131	7.6	367	1 OZZQMY	circumsporozoite p
9	127	7.3	1084	2 B64088	hemoglobin-binding
10	126.5	7.3	849	2 S61962	probable membrane
11	126.5	7.3	4152	2 T31102	filamentous hemagg
12	126.5	7.3	4919	2 T31105	hypothetical prote
13	126	7.3	631	2 S70910	transferrin-bindin
14	125.5	7.2	1036	2 S73601	protein P200 - Myc
15	122.5	7.1	1010	2 T13167	Lola-like protein
16	122	7.0	599	1 A64235	cytochrome-c-acces
17	121	7.0	1306	2 S22624	aggregation protei
18	120	6.9	604	2 D90523	lipoprotein [impor
19	119	6.9	773	2 F90537	lipoprotein [impor
20	118.5	6.8	782	2 A82940	hypothetical prote
21	117	6.7	395	2 JC5975	aurora-related kin
22	116.5	6.7	298	2 H64625	type I restriction
23	116	6.7	488	2 B91003	transferrin-bindin
24	115.5	6.7	682	2 F30603	vipe-like [mycopla
25	115	6.6	237	2 S46934	microfilarial shea
26	113.5	6.5	375	2 T08134	oleosin-like prote
27	113	6.5	791	2 C82940	hypothetical prote
28	112.5	6.5	430	2 JC2301	hypothetical 47.8k
29	111.5	6.4	366	2 T26449	hypothetical prote

conserved hypothet
cylicin I - human
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable membrane
probable membrane
hypothetical prote
hypothetical prote
X-linked PEST-cont
RNA-binding protei
ORF MSV230 hypothe
protein R52.2 (imp
FmtB protein [impo
aurora-related kin
serine-repeat anti

ALIGNMENTS

RESULT 1

PCSOAG
IgA Fc receptor precursor - Streptococcus agalactiae
N/Alternate names: beta antigen
C/Species: Streptococcus agalactiae
C/Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: S15330; S20240; S17038
R/Jerlstroem, P.G.; Chhatwal, G.S.; Timmis, K.N.
Mol. Microbiol. 5, 843-849, 1991
A/Title: The IgA-binding beta antigen of the c protein complex of Group B streptococci
A/Reference number: S15330; MUID:9131212; PMID:1857207
A/Accession: S15330
A/Molecule type: DNA
A/Residues: 1-1164 <JER1>
A/Cross-references: UNIPROT:P27951; EMBL:X59771
A/Accession: S20240
A/Molecule type: protein
A/Residues: 38-48 <JE2>
R/Jerlstroem, P.G.
submitted to the EMBL Data Library, August 1991
A/Reference number: S17038
A/Accession: S17038
A/Molecule type: DNA
A/Residues: 1-914, 'E', 916-1164 <JE3>
A/Cross-references: EMBL:X59771; NID:946522; PIDN:CMA42442.1; PID:G46523
C/Suprafamily: IgA Fc receptor
C/Keywords: Cell wall; immunoglobulin receptor; tandem repeat; transmembrane protein
F:1-37/Domain: signal sequence #status predicted <SIG>
F:38-1164/Product: IgA Fc receptor #status experimental <MAT>
F:199-438/Domain: IgA binding #status predicted <IGAL>
F:439-826/Domain: IgA binding #status predicted <IGR2>
F:827-945/Region: proline-rich repeats
F:946-1131/Domain: cell wall-spanning #status predicted <CWS>
F:1132-1159/Domain: transmembrane #status predicted <TMW>

Query Match 10.2% ; Score 177; DB 1; Length 1164;

Best Local Similarity 23.6% ; Pred. No. 0.0023;

Matches 81; Conservative 44; Mismatches 114; Indels 104; Gaps 15;

QY	12	TENHPKPVLPVPTQNNLQANVPQANASQANAPQANAPQANAPQANAPQANAPQ	71
DB	829	TDTFKIPQLPQADTPQADTPHVPESPKAPEAPRVPESPKTPEAPHVSPSPKAPAPR	888
QY	72	VENAPCAEVTVPVQ-----PQSQIDGDFDKIGSVKLNKEAQTLSRFTLVDLKGTTPK	127
DB	889	VPEPKTPEAPHVSPSPKTPPEAPKIP-----KPKPTDPVKLPDVPKLPDVPK	936
QY	128	-----FDKVSGR---KIIEEK--DFLVLNLSIDINAEQLSGDFLIIRS	164
DB	937	LPDAPKLPGLNKGAVGTSTDGNTKVTVPDKPTDADKHLKEVTTKELADKIA----	992
QY	165	DDLFGYGYHDTNGKNLVDAADKFSQVYVVD-----EKRVNDNISDKLTATYRKKEG	216

QY 55 ---QNAPOVENAQAQNAPOVENAQAQVTPVPVPOQSQIDGSPKIGSVKLNKEAQTLL 111
Db 121 TFPNVAPLYNA--TGPAPVNGQP-----PPGIESQWKYIDNSNGNIQFPFGNNNSQY 174
QY 112 ELSRFT---LVDKLGTPPKPKDKVSGKKI-IEEKDFVLNLSLDINAEQLSGDFLIRR---- 163
Db 175 QGGYFTPTLQICRLATSPBPFGVNDRFIRLGEITLVNNYQD---PFVAFDIVIRALNA 231
QY 164 -----SDDLIFY-----GYVHDT-----NGKNL 180
Db 232 VPLVAPTSSSKQKVESRDLPFVADVHSDDPTEYBEIILGLKFEDGSSYHETQVWVPVDGRHI 291
QY 181 --VDAADKFSQYFVWDEKRVNINISDKLTATYRKKEGFGYVGNPHTKFAARISKLGDV 238
Db 292 TKVDTRPKISAYTAPIS---TTSRKNKITSHEKV-----PSHBEASPE-----EQ 336
QY 239 EIKFNGQAQSGIKDEKQGNAEFTIKGDTKQLEI---TPTESN-----RI 281
Db 337 EVFSEEGRTVSNITNEES-----IVKNPTKQEEESRSGEKEQNILDQVQPEIEEDVKD 391
QY 282 IIAILDONQKSYTPGM-----EKALMETKFIKSKAGNSDKYLIQGEAKSDNWAQIM 332
Db 392 VISTADEPKSKDTPQMTSEQKRFAXAELMAQKLLBEQORQBEK-----KRRBEQRKL 445
QY 333 VSEKK 337
Db 446 KKEKK 450
RESULT 11
T31102
filamentous hemagglutinin 1 - Haemophilus ducreyi
C:Species: Haemophilus ducreyi
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31102
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A:Reference number: 220984; MUID:99030326; PMID:9811662
A:Accession: T31102
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4152 <WAR>
A:Cross-references: UNIPROT:Q9ZHL3; EMBL:AF057695; NID:g3929017; PID:g3929018; PIDN:AAC7
C:Genetics:
A:Gene: lspA1
Query Match 7.3%; Score 126.5; DB 2; Length 4152;
Best Local Similarity 21.4%; Pred. No. 18;
Matches 82; Conservative 61; Mismatches 130; Indels 111; Gaps 19;
QY 13 PNHKPKVLVPTKTONNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPOAQNAPOV 72
Db 2580 PEDAPPALPRTQSLIDSTEVPYSRSALANVKFDDASPMQ-----PSALRSKAF 2629
QY 73 ENAPOAEVTP-----PVPOQSOKI---DGSFDKIGSVKLNKEAQTLELSR 115
Db 2630 ADEPSE--TPKSRGKGISEESLSSTVQPSRSKISEEDSSFERLPLRIIDNGSDYAEILP 2688
QY 116 FTLVDKLGTPPKPKDKVSGKKIIEKDFVLNLSLDINAEQLSGDFLIRRSD---LFVGY 172
Db 2689 RNV--KQTNPEATQAIRAPALDN-----NDVIAERPS--FKRLQDLDVSVNGIY 2736
QY 173 HDTNGKNLVDAADKFS-QYFVVYDEKRVND-----NISDKLTATYRKKEGFGVY 219
Db 2737 SSIKPKALIEBGTPIRQVKTQVETPTDLVNKRELKVEDRSLLDKVQDTF----- 2788
QY 220 GSNPHTEKFAARISKLGDV-----EIKFNGQAQSGIKDEKQGNAEFTIKGDTKQ 270
Db 2789 -----QPLKVR-SKINDVRSSVEEYGGVTFKYAQSGEVYNEIVKHAE-----TQN 2834
QY 271 LEITPTESNRITIIAILDON-----OKSYTPGMEKAIME-----TKFIDSKAGNSD 315

Db 2835 GVCATCSHWTAKKVNDENIWTDLYKDGQGRKGLNKDAIESIEKLTQTEFIN--AGTAT 2892
QY 316 QKYLIGEAKSDNW---QAIMVSEK 336
Db 2893 QQFKL-----TNTWLEEQGVVPKQK 2912
RESULT 12
T31105
hypothenical protein 2 - Haemophilus ducreyi
C:Species: Haemophilus ducreyi
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31105
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A:Reference number: 220984; MUID:99030326; PMID:9811662
A:Accession: T31105
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4919 <WAR>
A:Cross-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC7
C:Genetics:
A:Gene: lspA2
Query Match 7.3%; Score 126.5; DB 2; Length 4919;
Best Local Similarity 21.4%; Pred. No. 22;
Matches 82; Conservative 61; Mismatches 130; Indels 111; Gaps 19;
QY 13 PNHKPKVLVPTKTONNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPOAQNAPOV 72
Db 2709 PEDAPPALPRTQSLIDSTEVPYSRSALANVKFDDASPMQ-----PSALRSKAF 2759
QY 73 ENAPOAEVTP-----PVPOQSOKI---DGSFDKIGSVKLNKEAQTLELSR 115
Db 2759 ADEPSE--TPKSRGKGISEESLSSTVQPSRSKISEEDSSFERLPLRIIDNGSDYAEILP 2817
QY 116 FTLVDKLGTPPKPKDKVSGKKIIEKDFVLNLSLDINAEQLSGDFLIRRSD---LFVGY 172
Db 2818 RNV--KQTNPEATQAIRAPALDN-----NDVIAERPS--FKRLQDLDVSVNGIY 2865
QY 173 HDTNGKNLVDAADKFS-QYFVVYDEKRVND-----NISDKLTATYRKKEGFGVY 219
Db 2866 SSIKPKALIEBGTPIRQVKTQVETPTDLVNKRELKVEDRSLLDKVQDTF----- 2917
QY 220 GSNPHTEKFAARISKLGDV-----EIKFNGQAQSGIKDEKQGNAEFTIKGDTKQ 270
Db 2918 -----QPLKVR-SKINDVRSSVEEYGGVTFKYAQSGEVYNEIVKHAE-----TQN 2963
QY 271 LEITPTESNRITIIAILDON-----OKSYTPGMEKAIME-----TKFIDSKAGNSD 315
Db 2964 GVCATCSHWTAKKVNDENIWTDLYKDGQGRKGLNKDAIESIEKLTQTEFIN--AGTAT 3021
QY 316 QKYLIGEAKSDNW---QAIMVSEK 336
Db 3022 QQFKL-----TNTWLEEQGVVPKQK 3041
RESULT 13
S70910
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB32)
C:Species: Haemophilus influenzae
A:Variety: strain SB32
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70910; S73323
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70910
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA

A;Residues: 1-631 <LOO>
A;Cross-references: UNIPROT:Q48043; EMBL:U15057
A;Experimental source: strain SB32, clone DS-1047-4-10
R;Loosemore, S.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241, 'P', 243-420, 'C', 422-508, 'A', 510-631 <LOW>
A;Cross-references: EMBL:U15057; NID:g1223952; PIDN:AAC43933.1; PID:g1223953
A;Experimental source: strain SB32, clone DS-1047-4-10
C;Genetics:
A;Gene: cbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 7.3%; Score 126; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 1.7; Mismatches 45; Indels 70; Gaps 14;
Matches 67; Conservative 45; Mismatches 45; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPFPVFPQ-----SOKIDGSPDKIGSVKLNKEAQTLELSRFTLVKDL 122
Db 322 VFSAKETEKPPLKRETLIDGLKTTFTSKTDTTNTKITSKNTPE-----NFTTKD-- 372

QY 123 GTPPKFDKVSCKKIEEKDFVLNLSDNAEQLSGDLFIIRSDLLFYGYVHTNGKLV-V 181
Db 373 --IPSFG-----EADYLLIDNPYLPPLPSGDFRISK-----RHEVGGRKYV 413

QY 182 DAADK---FSQYFVVYDSEKRVNDNISDK-----LTATYRKKEGFGVYGSNPHTKFEFAARIS 233
Db 414 EACCKNLVSVFEGMYEDKENNETDKKEKQTTTSIKYVQLLGLRTPSSE----IP 469

QY 234 KLGDEVIKFGNQAGSKIDKQGNAEFTTKGTQKLEITPTESNRILIIAILDONOKSY 293
Db 470 KMGNTYR---GSWFGYIGDDKTS---YSATGKRQDKNAPAEFN-----VDFNNKKL 516

QY 294 TPGVEKAIMETKFTIDSKA-----GNSDKYLLIGAKSDNW 328
Db 517 TGTSKRHDNQVPVFNKATFNGRNDPE---GTATAENF 552

RESULT 14
protein P200 - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: cyradherence-accessory protein (hmw1) homolog; hypothetical protein P
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
A;Accession: S73601; S49062
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73601
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1036 <HM>
A;Cross-references: UNIPROT:P75211; EMBL:AE000027; GB:U00089; NID:g1673941; PIDN:AAB9592
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
R;Proft, T.; Herrmann, R.
Mol. Microbiol. 13, 337-348, 1994
A;Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae
A;Reference number: S49059; MUID:95075318; PMID:7984111
A;Accession: S49062
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: P, 642-678 <PRO>
A;Cross-references: EMBL:Z32646; NID:g474071; PIDN:CAA83569.1; PID:e104325; PID:g1333782
A;Experimental source: clone D2-1C-Alu
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
C;Genetics:

A;Genetic code: SGC3

Query Match 7.2%; Score 125.5; DB 2; Length 1036;
Best Local Similarity 20.2%; Pred. No. 3.4;
Matches 77; Conservative 65; Mismatches 123; Indels 117; Gaps 20;

QY 9 SSSTPN-HPKPVLPVKTQNNLQANVPOAQNASQAQNAPOAQNAPQANAPQAVENAPQAA 67
Db 703 TESDFSEFEVEIQEPFNFDELTIPEPSELTETE--PEPNFEFEVELEPEIENFESE 760

QY 68 NAPAQVENAPQAEV-TPVPV-----OPQSO---KIDGSPDKIGSVKLNKEAQT----- 110
Db 761 TEVQQLAQESSFSEPEFNFTEVEVQPESEIESEKFEAEVQSEPKVSLNSDFETKPEAQ 820

QY 111 LELSFTL-VKLGTPPKFD-KVSGKKIIEKDFVLNLSDNAEQLSGDLFIIRSDLLF 168
Db 821 ABVTPTLEATEATSEAPQLPTEATKVVD-----DVEEQDLWELLIGNSN--- 867

QY 169 YGYH-----DTNGKLVDAADKFSQYFVVYDEKRVNDNISDKLTATY-RKKEG 216
Db 868 YGYHPSGSEWVAGVFDNQNITWTPDASVEWAR-----ESDYTLDIGEITVGRYRKGEW 921

QY 217 FVYGSNPHTKFEA-----ARISK-----LG-----DVEIKFENGQAQGS 250
Db 922 IWGYVDETGEWLVDEHYQNHQPRISEAPRFWEQLIGNEDYGYVEDNWKWYDGEF--- 978

QY 251 IKDEKQGNAEFTIKG--DTKQLEITPTESNRILIIAILDONOKSYTPCWKAKIMETKFD 308
Db 979 ---DSEGNLVFHSNAEDAKNIDI-----AKDIPVFESFDVD 1013

QY 309 S-----KAGNSDKYLLIGE 322
Db 1014 SIDADEWLDDQFSDSDAKEVFG 1035

RESULT 15
T13167
Lola-like protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13167
R;Cavarec, L.; Jensen, S.; Casella, J.P.; Cristescu, S.A.; Heidmann, T.
Mol. Cell. Biol. 17, 482-494, 1997
A;Title: Molecular cloning and characterization of a transcription factor for the copia
A;Reference number: Z17624; MUID:97127405; PMID:8972229
A;Accession: T13167
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1010 <CAV>
A;Cross-references: UNIPROT:O18346; EMBL:Y14994; NID:g2467111; PIDN:CAA75228.1; PID:g2467
C;Genetics:
A;Cross-references: FlyBase:FBgn0022628
F;18-119/Domain: POZ domain homology <POZ>

Query Match 7.1%; Score 122.5; DB 2; Length 1010;
Best Local Similarity 21.9%; Pred. No. 5.1;
Matches 70; Conservative 47; Mismatches 118; Indels 85; Gaps 14;

QY 1 CGSGSGSGSSSTPNHPKPVLPVKTQNNLQANVPOAQNASQAQNAPOAQNAPQANAPQAV 60
Db 257 CGSSSGSGSOVTNQ-----PLTSSSSSSNVTKTESAKLTSTAAGGAQGGQQQQQQQ 309

QY 61 ENAPQANAPQVENAPQAEVTPVPVPOQSQKIDGSFDKI-----GSVKLNKEAQT 111
Db 310 QTSSDAINTENVQ-----QQNQCAQGDAAEMDVASGGAASGAVAVHFGV--- 355

QY 112 ELSRFTLVKLGTPPKF-DKVSQKKIIEK-----DFVLNLSDNAEQL--- 155
Db 356 -VKQUTTLIDKSNHKKQIKDNIITTEWIEPKAEYDDDDAHDENVEDLILDEEDYTWELDQ 414

QY 156 -----SGDFLI-----RRSDLLFYGYVHTNGKLVDA-ADKFSQYFVVYDEKRV 199
Db 415 AAGTSQGGSGSSQAVATWQHDRSQDELGLMAAQQRDPQDAKQKQEGTEGAHDEFEL 474

QY 153 FQLSGDFLIRSDDLFYGYHDTNGKNLVDAADKESQYFVYVYDKRVN-----DN 202
DB 241 EKISSTLLTKK-----EGNN-----ESKQINFETEKSRIOKNS 273
QY 203 ISDKLTATYRKEGVYSGNSPHTKFAARISKLGDBVIKFN-----GQAQGSIKDE 254
DB 274 LKDLQTKWKISQ-IKFNASSYTPLDGSF-----DYKSSFEYNRIKEILLTSLNFSYKEE 328
QY 255 KGNABEITIKGDTKQLBEITTEENRIIALLDONQKSYTPGMEKAIMETKFDISKAGNS 314
DB 329 KKHILSFSEKSSDFNLGLLAKGDNF-----GPFKETLESKEI-----SDI 371
QY 315 DOKYLIGEAKSDNWQAIMVSEKK 337
DB 372 DQITFSPDKD-----AVGEKR 389

RESULT 25
S46964
Microfilial sheath protein - nematode (Brugia malayi)
C:Species: Brugia malayi
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S46964
R:Hintzmann, J.; Schnauffer, A.; Hintz, M.; Conraths, F.J.; Stirm, S.; Zahner, H.; Hobom, submitted to the EMBL Data Library, July 1994
A:Description: Brugia spp. and Litomosoides carinii: characterization of the shp2 gene
A:Reference number: S46964
A:Accession: S46964
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <HIR>
A:Cross-references: UNIPROT:Q17242; EMBL:Z35444; NID:G5163352; PID:G5163353
C:Genetics:
A:Introns: 26/1
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 6.6%; Score 115; DB 2; Length 237;
Best Local Similarity 23.8%; Pred. No. 2.4;
Matches 43; Conservative 12; Mismatches 60; Indels 66; Gaps 5;

QY 10 SSTNHPKPVLPVKTQNNLQAVPOQANASCAQNAPOQANAPQAVENAPQAVNAPOQNA 69
DB 118 SQYFWPQPPQYQ-----LPQYTOPQYQALQYQPAQYQPAQYQPAQYQPAQYQPA 168
QY 70 PQVENAPQAVTPPVPOQSQKIDGSDFKIGSVKLNKEAQTLESLRFTLVKLTGTPPKFD 129
DB 169 PQYQVQYQPPQYQPPQYQ-----PPQYQ 194
QY 130 KVSCKKIIEKDFLVNLSDINAEQLSGDFLIRSDDLFYGYHDTNGKNLVDAADKFSQ 189
DB 195 KA-----SKYPQYPTAGAGMVGSS-----LYGIVEEDSDQLTD-----FEQ 231

QY 190 Y 190
DB 232 Y 232

RESULT 26
T08134
oleosin-like protein - rape
C:Species: Brassica napus (rape)
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08134
R:Hong, H.P.; Ross, J.H.; Garster, J.L.; Rigas, S.; Datla, R.S.; Hatzopoulos, P.; Scoles Plant Mol. Biol. 34, 549-555, 1997
A:Title: Promoter sequences from two different Brassica napus tapetal oleosin-like genes
A:Reference number: Z16373; MUID:97369377; PMID:9225865
A:Accession: T08134
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-375 <HON>
A:Cross-references: UNIPROT:P93066; EMBL:Y09986; NID:g1769971; PIDN:CAA70173.1; PID:g176

A:Experimental source: cv. Jet Neuf
C:Genetics: 105/2; 184/2
A:Introns: 105/2; 184/2

Query Match 6.5%; Score 113.5; DB 2; Length 375;
Best Local Similarity 29.6%; Pred. No. 5.3;
Matches 45; Conservative 9; Mismatches 69; Indels 29; Gaps 4;

QY 2 GSGSGSSSTNHPKPVLPVKTQNNLQAVPOQANASCAQNAPOQANAPQAVENAPQAVNAPOQVE 61
DB 181 GKGRHMGVNPENPPGAPPTGPPAPAAPEAPAAAPAAAPAAAPAAAPAAAPADDP 240
QY 62 NAFQANAPQAVENAPQAVTPPV-----POPSQKIDGSDFKIGSVKLNKEAQTLESL 114
DB 241 AAPAAPEAPATPAAPAPAAAPAAAPAAAPAAAPAAAPPPPSF-----LSLLEMP 289
QY 115 RF---TLVDKLTGTPPKFKVS-----GKK 135
DB 290 SPIKSKLIEALINIFGFKKSNDRGKSGGKK 321

RESULT 27
C82940
hypothetical protein U0046 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82940
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A:Reference number: A82870
A:Accession: C82940
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-791 <GLA>
A:Cross-references: GB:AE002104; GB:AF222894; NID:G6898990; PIDN:AAF30451.1; GSPDB:GNC011
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: U0046
A:Genetic code: GGC3

Query Match 6.5%; Score 113; DB 2; Length 791;
Best Local Similarity 19.7%; Pred. No. 15;
Matches 69; Conservative 57; Mismatches 122; Indels 102; Gaps 18;

QY 12 TPNHPKPVLPVKTQNNLQAVN-POANASCAQNAPOQANAPQ--AQANAPQAVENAPQAVNA 68
DB 88 TP-FPDPIPTPKBELKPKPEIKPEPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 146
QY 69 AQVENAPQAVTP-PVPOQSQKIDGSDFKIGSVKLNKEAQTLESLRFTLVKLTGTPP 126
DB 147 LPSPSPPKPEPKPPDPDPQPPQPPQ--STVRKIELNG-----VLVDAAVEVPP 195
QY 127 -----KFDKVSCKKIIE-----EKDFLVNLSDINAEQLSGDFLIRSDDLFYGY 171
DB 196 PRQTFKYDQDGLSNLNPYTNISVGKIKKVFVDELHRKSDLVKGN-LKRGD----- 247
QY 172 YHDTNGKNLV-----AADKFSQYFVYVYDKRVNDNISDKLTATYRKEGVYSGNSPHTKF 228
DB 248 -YQSLVKOLLDPNPKPEIDSYIANVD-----KSGY-----HAKLW 282
QY 229 AARISKLGDE--IKFENGQAQGSIKDEK-----DGNAEI 261
DB 283 -SKFKLLFDTNVNVLNFKQKKEYPNMTKTVSDAHKAYMLYAHLDPSKTKLSANSEK 341
QY 262 FTIKGDTKQLEITPESNRRIIALDQNKQSYTPGMEKAIMETKFDISKA 311
DB 342 YLQEG-----LTPDPDPSYVNGELDSYAYSPAKETNTVTSLANDNA 385

RESULT 28
JC2301
hypothetical 47.8K protein - Pneumocystis carinii

N;Alternate names: CRP-3
C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: JC2301
R;Wada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:36051989; PMID:8535973
A;Accession: JC2301
A;Molecule type: DNA
A;Residues: 1-430 <WAD>
A;Cross-references: UNIPROT:Q01823; GB:D31909; GB:D17441; NID:G559718; PIDN:BAA06706.1;

Query Match 6.5% Score 112.5; DB 2; Length 430;
Best Local Similarity 30.0%; Pred. No. 7.3;
Matches 27; Conservative 13; Mismatches 37; Indels 13; Gaps 2;

Qy 6 SGSSSTPNHPKVLVPTQNLLQAQNVPAQASQAQNAPOAQNAPOAQNAQVENAPQ 65
 | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 249 STSSEPPPPPPPRPEPQC-----PETQPETQPPQPPQPPQSETQTETOPEE 300
 | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 66 AQNAQVENAPQAEVTTP-----VPQPQSQ 90
 | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 PRRPPEPPEPEPQQPVQSVPPQPPETOQ 330
 | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 29
T26449
T26449
hypothetical protein Y113G7B.23 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26449
R;Lennard, N.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20215
A;Accession: T26449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-366 <WIL>
A;Cross-references: UNIPROT:Q9U2W6; EMBL:AL110477; NID:e1542121; PIDN:CAB54337.1; CESP:Y
C;Genetics:
A;Gene: CESP:Y113G7B.23
A;Introns: 318/1

```

Query Match      6.4%; Score 111.5; DB 2; Length 366;
Best Local Similarity 28.3%; Pred. No. 6.9;
Matches 28; Conservative 1%; Mismatches 34; Indels 25; Gaps 2;

Qy 16 PKPVLVPTQNNLQAQNVFQAQNASQAQNPQAQNAPOQNAPOVENAPOQNAPOVENA 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 139 PQP--TFQVQISAEAAIPEKMDTSEATRAARPPSTQAPCAPFPVQAAPFVQAPOQA 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 76 P-----QAEVTPPVFPQSQK 91
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 PPOAYQYGGPGGPPQAYRYPPQGGQYSPYPPPPQQQ 235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 30
A90575
conserved hypothetical protein MYPU_05050 [imported] - Mycoplasma pulmonis (strain UAB CT
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: A90575
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: A90575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-833 <KUR>
A:Cross-references: UNIPROT:Q98063; GR:A14455566; PDB:1G10489919; PDB:CACI3678.1; GSPDB:G

A;Experimental source: strain UAB CT1P
C;Genetics:
A;Gene: MYPU_5050
A;Genetic code: SGC3

Query Match 6.4%; Score 111.5; DB 2; Length 833;
Best Local Similarity 20.3%; Pred. No. 20;
Matches 92; Conservative

Qy 20 LVPTKTNLQAQ-----NVPQAQNASQAQAPQAQAPQAQAPQAQAPQAQAPQAQAP 70
Db 56 LIPK--NNLDYRQAAPTDFNLPEIQERLPEPEKPEEPQPLPEPEPEKPEKPEKPEP 113
Qy 71 QVENAPQAEVTPVPVQPSQKI-----DGSF-DKI---GS 101
Db 114 KPAPLPKEIPKPIPKPQPKPLPPQPKVEFPKTPPIRQSKPSDEAKEGQIVDKIVKFGG 173
Qy 102 VKLN---KEAQTUELSTFTLVKLG-----TPPKFDK-----VSGKK 135
Db 174 VDIKVKVTRTPRTRKVSQKIDDKIANRPNRYNDIADHIVSAEVTPEYIEKRNQRLKGLK 233
Qy 136 --IIEKDFL-VNL--SDIN--AEOLSG--DFLIR----- 162
Db 234 QNFLANQNFPLNLLNAKESDVYKIADHLAGNPTFFYRVIAKFKQLDDPNVWPNLHNR 293
Qy 163 --RSDLFYGYHYDTNGKLVDAADKFSQFVVYDE-----KRVNDNIS--DKLTA 209
Db 294 DYRGD-----DTPDPNL--ELQKFLKNGYTLDDVKKLABIKXKIQEVVDYDYPYAK 343
Qy 210 TYRKKEGFVYGSN-----PHTKEFAAR-SKLGDVFI--KFENGQAQ-----GSIKDEK 256
Db 344 DPRKKIKCYGPNCFEGKKGHVLEYIRINIMDTNLTFLKLDSENTQDIRKGYVIDEEN 403
Qy 257 GNABEFTIKGDTKOLEITPTESNRILIALDQNK-----SYTSGM 297
Db 404 DNVFI-NSKGEINSYSKAPLINGTKILYKXONTERRAFGYSSNMWRFGQIGESY-PGW 461
Qy 298 EKATMEI-----KFIDSKAGNSDKYLGIAKSD 326
Db 462 TKTDITTSPEYKYNVSKRGINISKULTRVKSQ 495

RESULT 31
B40713
Cylicin I - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: B40713; S35920
R;Hess, H.; Heid, H.; Franke, W.W.
J. Cell Biol. 122, 1043-1052, 1993
A;Title: Molecular characterization of mammalian cylicin, a basic protein of the
A;Reference number: A40713; MUID:93359502; PMID:8354692
A;Accession: B40713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-598 <HSS>
A;Cross-references: UNIPROT:P35663; GB:222780; NID:G396104; PIDN:CAA80457.1; P
C;Keywords: cytoskeleton

Query Match	6.4%	Score 111;	DB 2;	Length 598;	
Best Local Similarity	21.6%;	Pred. No. 14;			
Matches	79;	Conservative 51;	Mismatches 142;	Indels 94;	Gaps 16
QY	7	GGSSSTPNHPKFLVLPKTNLQKNQVNP--QAQNASQAQNAPOAQNAPQNAQPOVENA	63		
		:::	:::	:::	:::
Db	82	GGSYATNPESQIIVEEKTQRQNEADKTPLKSSHENEQSKSSSETNPSONSKTV--	138		
		:::	:::	:::	:::
QY	64	POAQNAPQVENAPOAEVTPFPVPOSQKDGSFDKIGSVKLKKAQTLELSRFTLVLDKLG	123		
		:::	:::	:::	:::
Db	139	--SKNCSQDKKK-----DSKSKKNTNTEFLTK-----	164		
		:::	:::	:::	:::
QY	124	TPPFPD---KVSQKKIIEKDFLVNLSDINAEQLSGDFTLRSSDDLFYGY-----YH	173		
		:::	:::	:::	:::

A:Molecule type: DNA
A:Residues: 53-164, 'STSTSGSSSSNATESGSSVSGTSTATSGSSNAGSS', 166-186, 'V', 188-286, 745-773; 781;
A:Cross-references: EMBL:X89715
C:Genetics:
A:Cross-references: SGD:S0005515
A:Map position: 15L
A:Note: YOL155c

Query Match 6.4%; Score 110.5; DB 2; Length 967;
Best Local Similarity 19.2%; Pred. No. 28;
Matches 78; Conservative 55; Mismatches 160; Indels 113; Gaps 14;

QY 6 SGGSSSTPNHPKPLVLPKTNQLQAQNVPOAQNASQAQNAPOACNAPO-----AQN 56
DB 222 SGASSVPSSGSGVTESSGSSSASESITQGTASGSSASSTGSGVTQSGSSVSGSSASS 281
QY 57 APOVNA-POAQNAPO-----VENAPQAEVTPP-----VPOQSQ 90
DB 282 APGISSTPQSTSSASTASGSIITSGTLLSSITSSASSATATASNLSSDGTIYLP---ST 338
QY 91 KIDGSPDKIGSVKLKEAQTLELSRFTLVDPKLTGTPPKFDKVSQKIIIEKDELVLNLSDI 150
DB 339 TISGDTLTGSIATEAVEAAGKILFLD-----GDKYVFSADFII--- 380
QY 151 NAEQLSGDFLIRRSDDLFYGYHDTNGKUL-----VDAADKFSQYFVVYDEKRVND 201
DB 381 ----HGVVFVSKSPYPTGTEFDISGENFDVSGTFNAEPPAASSAYSFTPGSPFNSG 435
QY 202 NISDKLTATYRKKEGFGVYGSNPHTKFAAARISKLDV-----BIKPENG- 245
DB 436 DISLSLSESTKGEVTFSPYNSGAFSPSNAILNGSVSGLQRRABSGSVNNGEINLENGS 495
QY 246 -----QAQGSIK-----DEKQNAEIFIKGDTKOLEITPTESNRI----II 283
DB 496 TVVVVPEVPSGSGTINIISGNLYLHVPDTFTGQTVVFKGEG---VLAVDPTEITWTPIPV 552
QY 284 AILDONQKSYTPGMEKAIME--TKFIDSKAGNSQDKYLIGEAKSDN 327
DB 553 GYTGENQIATADVTALSYDSATGLVLTATQNSQSFSGTGFSS 598

RESULT 35
S67803
probable membrane protein YDL239c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein D0771
C;Species: *Saccharomyces cerevisiae*
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67803
R;Alt-Moerbe, J.; Schneider, C.; Moro, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67798
A;Accession: S67803
A:Molecule type: DNA
A:Residues: 1-790 <ALT>
A:Cross-references: UNIPROT:Q07732; EMBL:Z74287; NID:G1431405; PID:e253369; PID:g1431406
A;Experimental source: strain S288C
C:Genetics:
A;Gene: SGD:ADY3; MIPS:YDL239c
A:Cross-references: SGD:S0002398
A:Map position: 4L
C;Keywords: transmembrane protein
F;706-722/Domain: transmembrane #status predicted <TM>

Query Match 6.3%; Score 110; DB 2; Length 790;
Best Local Similarity 19.3%; Pred. No. 23;
Matches 78; Conservative 73; Mismatches 145; Indels 108; Gaps 16;

QY 4 SGGSSSTPNHPKPLVLPKTNQNN-----LQAQNVPOAQNASQAQNA----- 44
DB 90 SWAGSEASPNGNISTLENATEKTKLPNKFLQGGGLPTVIGISQALSPAGKSTILGNV 149
QY 45 APOQNAPOAQNAPOV-----ENAPQNAPOQVEN 74

Db 472 VNIRQTQSKQEIENNG:PMKKAETTEEDSENPQWQNSQFIRDMIMKNSDKVEYKI 531
QY 172 YHDT-----NCKNLV----- 181
Db 532 VHDDPASDDILNHNHNGSALLIEVFTALLRLFINERGDWSCIIVENWIIDDKGVLMERK 591
QY 182 -----DAADFQSFQVYVYDEKRVNDNISDKLTATYRKKEGFVYSGNPHTKFEFAARISKL 235
Db 592 DERGEGEAKQRNAHGYFLQDKKIDNLKDTL-----KENATEVQKE 633
QY 236 GDV--EIKFENGQAGSKTKDKGNNAEFTIKGTQKOLE-ITPTESNR-----IIIAILD 287
Db 634 SDAKNETNSDSKSDSDSEERDPKLEKLNRYNVNMIERTKQFNNSYWLIIILGLVLE 693
QY 288 QNQSXYTPGMEKATMETKFIDS 309
Db 694 DCR--HLP-----MYTEFIDS 707
RESULT 37
B90580
hypothetical protein MYPV 5460 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B90580
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: B90580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1216 <CUR>
A:Cross-references: UNIPROT:Q98023; GB:AL445566; PID:g14089961; PIDN:CAC13719.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV 5460
A:Genetic code: SGC3
A:Superfamily: DNA-directed RNA polymerase beta chain
Query Match 6.3%; Score 109.5; DB 2; Length 1216;
Best Local Similarity 21.8%; Pred. No. 43;
Matches 78; Conservative 49; Mismatches 147; Indels 83; Gaps 18;
QY 16 PKPV-----LVPTQNNLQANVPOAQNASQAQANPQACNAPQANVPOQVNAPOQANVAPQ 71
Db 646 PREVDYIDVSSKQMTSLAASSIPFLEN-NDANRALMGSNM-QRQAVPLL-----FAEAPL 698
QY 72 VENAPQAEVTPPVQPOQSKIDGS--PDKIGSVKLKNEA-----QTLRLSRFTLVDPKLG 123
Db 699 VATGIEADIAKPSFNLLKSTVDGEVFGVDSQIKKDSASEKSGIKTYQLX----- 749
QY 124 TPKPKFVKVSGKKIIEEKDFVLNLSDNAEQLSGDFLIRSDDLFYGYHYHDTNGKNLVDA 183
Db 750 ---TFEKTNQGVTSQSP--IVKMGD---KVLKGDLI---SDSSSFMDGEMALCKNVLVG 798
QY 184 ADKFSQY----FVYVYDEKRVNDNI-----SDKLTATYRKKEGFVYSGNPHTKFEFA 210
Db 799 FSTWNGVNYEDAIIVSERLKVDDVFTSIHIEEQIQFRKSKAGDDKUTADIPNASLKR 858
QY 211 YRKKEGFV-YGSNPHTK-FAARISKLGDVEI----KFGNQAGSKTKDEKDGNAEFT- 263
Db 859 HLDENGIVRIGSEVVTGDLVGRVSPKGDENI SPAEKLNGIFNQKISNEKD--SLKVKNG 918
QY 264 IKGDTQKLEITPTESNRIIIAILDQNKSYTPGMEKAIMETKFIDSKAGNSDQKYLII 320
Db 919 HQTVIDVEILSRENGVNLLEEIDMTIKVYVAQKRK----IKVGDVAGRHGNGKVI 971
RESULT 38
T01512
hypothetical protein T10M13.12 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01512
R:Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gotte
Martensen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A:Reference number: Z14346
A:Accession: T01512
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1293 <JH>
A:Cross-references: UNIPROT:O04251; EMBL:AF001308; NID:g2104523; PID:g93912929
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4S
A:Introns: 29/3; 59/3; 94/3; 121/1; 144/2; 159/2; 1120/2; 1192/3
A:Note: T10M13.12
Query Match 6.3%; Score 109.5; DB 2; Length 1293;
Best Local Similarity 20.6%; Pred. No. 46;
Matches 71; Conservative 54; Mismatches 92; Indels 127; Gaps 15;
QY 68 NAPOVENAPQAEVTPP-----VPOQSQKIDGSPDKIGSVKLKNEAOTLELSRFTLVDPK 122
Db 621 SAPVTGNQKQISSPVLTVEVQDMAKHID-----TETEALQ----- 658
QY 123 GTTPPKFVKVSGKKII-EKDFVLNLSDNAEQLSGDFLIRSDDLFYGYHYHDTNGKNLV 181
Db 659 ----GIDSVDNKSAPKEKDLVLDLM-VNQDKLQA-----KTP 692
QY 182 DAADKFSQYFVYVYDEKRVND-----NISDKLTATYRKKEGFVYSGNPHTKFEFA 229
Db 693 EAADADEVEITVL--BRELVNPTDPSDQALQSEVDKTKRKRKEAGVGNKSLQGRKGS 750
QY 230 ARISKLGQVEIK-----FENG-QAQSIT-KDEKDGNA-----EIF 262
Db 751 SFTAKVGKSRVKKTKISRKENDIKANGTLKMGDGDNSADGKNLALHENGKVSQSGDQS 810
QY 263 TTGGDT-----KQLEITPTESNRIIIAILDQNKSYTPGMEKAIMETKF 307
Db 811 LVAGETLTRKEAATKDPYAAAQLEVDTKGKRRKQATVEEN-RLQTPSVKAKVSKKED 869
QY 308 DSKAGNSDQKYL-----IGEAKSDNMQAIMVSE 335
Db 870 GAKANTVKKDIWIHSAEKENVAVDNCGDVSSDGAQSLVVEK 913
RESULT 39
I39295
X-linked PEST-containing transporter - human
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I39295; I38495
R:Lafreniere, R.G.; Carrel, L.; Willard, H.F.
Hum. Mol. Genet. 3, 1133-1139, 1994
A:Title: A novel transmembrane transporter encoded by the XPC gene in Xq13.2.
A:Reference number: I38495; MUID:95072579; PMID:7981683
A:Accession: I39295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-613 <RES>
A:Cross-references: UNIPROT:P36021; EMBL:U05321; NID:g458253; PIDN:AAB60375.1; PID:g458282;
A:Accession: I38495
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 16-613 <RES>
A:Cross-references: EMBL:U05315; NID:g458246; PIDN:AAB60374.1; PID:g458247
C:Genetics:
A:Gene: XPC
A:Introns: 218/1; 266/2; 416/3; 464/3; 541/1
Query Match 6.3%; Score 109; DB 2; Length 613;

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OM protein - protein search, using sw model

Run on: December 17, 2004, 15:57:34 ; Search time 175.595 Seconds
(without alignments)
686.754 Million cell updates/sec

Title: US-10-696-544-2

Perfect score: 1734

Sequence: 1 CGSGSGSGSSPTNHPKPV.....YLIGAKSDNQAIWVSEKK 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1734	100.0	337	16	US-10-696-544-2
2	221.5	12.8	335	15	US-10-406-686A-41
3	219	12.6	43	16	US-10-696-544-12
4	186.5	10.8	1164	9	US-09-797-385-10
5	178.5	10.3	1104	9	US-09-797-385-4
6	177	10.2	1164	9	US-09-797-385-2
7	173	10.0	1128	9	US-09-797-385-6
8	168	9.7	1098	9	US-09-797-385-8
9	141	8.1	3164	17	US-10-669-161-72
10	140.5	8.1	730	9	US-09-748-875-68
11	140.5	8.1	730	10	US-09-238-523B-68
12	137.5	7.9	756	17	US-10-425-115-288440
13	135	7.8	94	16	US-10-767-701-56462

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14 132.5 7.6 447 14 US-10-156-761-9880 Sequence 9880, Ap
15 129.5 7.5 238 17 US-10-739-930-10816 Sequence 10816, A
16 129 7.4 409 16 US-10-771-931-33 Sequence 33, Appl
17 127 7.3 448 15 US-10-244-596-14 Sequence 14, Appl
18 125.5 7.2 1036 15 US-10-382-122A-64159 Sequence 64159, A
19 124.5 7.2 784 17 US-10-425-115-301016 Sequence 301016,
20 124 7.2 631 14 US-10-043-344-115 Sequence 115, App
21 122 7.0 599 15 US-10-382-122A-63567 Sequence 63567, A
22 121.5 7.0 1013 17 US-10-807-746-14 Sequence 14, Appl
23 121 7.0 315 17 US-10-425-115-281769 Sequence 281769,
24 120.5 6.9 287 17 US-10-758-846-20 Sequence 20, Appl
25 120.5 6.9 306 15 US-10-112-944-413 Sequence 19, Appl
26 120.5 6.9 306 17 US-10-758-846-19 Sequence 19, Appl
27 120 6.9 430 16 US-10-771-931-54 Sequence 54, Appl
28 118 6.8 334 9 US-09-789-054A-4 Sequence 4, Appli
29 118 6.8 334 16 US-10-628-969-4 Sequence 4, Appli
30 117.5 6.8 456 16 US-10-771-931-13 Sequence 13, Appl
31 117.5 6.8 646 17 US-10-425-115-230961 Sequence 230961,
32 117.5 6.8 806 16 US-10-771-931-9 Sequence 9, Appli
33 117.5 6.8 1009 15 US-10-771-931-7 Sequence 7, Appli
34 117.5 6.8 1046 16 US-10-771-931-1 Sequence 1, Appli
35 117 6.7 297 17 US-10-425-115-281772 Sequence 281772,
36 117 6.7 2478 9 US-09-815-242-5816 Sequence 5816, Ap
37 117 6.7 2478 9 US-09-815-242-12967 Sequence 12967, A
38 116.5 6.7 298 10 US-09-882-227-138 Sequence 138, Appl
39 116.5 6.7 459 17 US-10-702-305A-18 Sequence 18, Appl
40 116.5 6.7 704 16 US-10-437-963-1855221 Sequence 185221,
41 116.5 6.7 2497 14 US-10-161-051-189 Sequence 189, App
42 116 6.7 464 15 US-10-220-480-2 Sequence 2, Appli
43 116 6.7 488 16 US-10-220-481-84 Sequence 84, Appl
44 116 6.7 488 16 US-10-220-481-619 Sequence 619, Appl
45 115.5 6.7 340 9 US-09-789-054A-6 Sequence 6, Appli
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ALIGNMENTS

RESULT 1

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US-10-696-544-2
; Sequence 2, Application US/10696544
; Publication No. US20040156865A1
; GENERAL INFORMATION:
; APPLICANT: Confer, Anthony W
; APPLICANT: Ayalew, Sahu
; APPLICANT: Murphy, George
; APPLICANT: Pandher, Karamjeet
; TITLE OF INVENTION: M. Haemolytica Outer Membrane Protein plpE as a Vaccine or
; TITLE OF INVENTION: Vaccine Component Against Shipping Fever
; FILE REFERENCE: C0300-57188/02-744
; CURRENT APPLICATION NUMBER: US/10/696,544
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/422,305
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Mannheimia haemolytica
; PUBLICATION INFORMATION:
; AUTHORS: Pandher et al.
; TITLE: Genetic and Immunologic Analyses of PlpE, a Lipoprotein Important
; TITLE: In Complement-Mediated Killing of Pasteurella Haemolytica
; TITLE: Serotype 1
; JOURNAL: Infection and Immunity
; VOLUME: 66
; ISSUE: 12
; PAGES: 5613-5619
; DATE: 1998-12
; US-10-696-544-2
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Query Match 100.0%; Score 1734; DB 16; Length 337;
Best Local Similarity 100.0%; Pred. No. 2.2e-123;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAOVPOAQNAPQAOAQNAPQAOV 60
DB 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAOVPOAQNAPQAOAQNAPQAOV 60

QY 61 ENAPOAQNAPQAOVAPQAEVTPVPOQOSQKIDGDFKIGSVKLNKEAQTLESLRFLVD 120
DB 61 ENAPOAQNAPQAOVAPQAEVTPVPOQOSQKIDGDFKIGSVKLNKEAQTLESLRFLVD 120

QY 121 KLGTTPKPKDKVSGKKIIEBKFLVNLSDINAEOLSGDFLIRSDDLFYGYHDTNGKNL 180
DB 121 KLGTTPKPKDKVSGKKIIEBKFLVNLSDINAEOLSGDFLIRSDDLFYGYHDTNGKNL 180

QY 181 VDAADKFSQYFVYDEKRVNDSKLTATYRKKEGVYGSNPHTKFAARISKLGDVEI 240
DB 181 VDAADKFSQYFVYDEKRVNDSKLTATYRKKEGVYGSNPHTKFAARISKLGDVEI 240

QY 241 KPEQAQGSINDEKXGNAEFTTKGDTKOLEITPTESNRRIIAILDQNKSYTPGMEKA 300
DB 241 KPEQAQGSINDEKXGNAEFTTKGDTKOLEITPTESNRRIIAILDQNKSYTPGMEKA 300

QY 301 IMETKFKIDSKAGNSDKYLIKEAKSDNQWQAIMVSEK 337
DB 301 IMETKFKIDSKAGNSDKYLIKEAKSDNQWQAIMVSEK 337

RESULT 2

US-10-406-686A-41
; Sequence 41, Application US/1040686A
; Publication No. US20040033586A1
; GENERAL INFORMATION:
; APPLICANT: CROCKE, HELEN RACHEL
; APPLICANT: SHEA, JACQUELINE ELIZABETH
; APPLICANT: FELDMAN, ROBERT GRAHAM
; APPLICANT: COUTEBROZE, SYLVAIN GABRIEL
; APPLICANT: LEGROS, FRANCOIS-XAVIER
; TITLE OF INVENTION: ATTENUATED GRAM NEGATIVE BACTERIA
; FILE REFERENCE: 454313-3171.1
; CURRENT APPLICATION NUMBER: US/10/406,686A
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/370,282
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 41
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-406-686A-41

Query Match 12.8%; Score 221.5; DB 15; Length 335;
Best Local Similarity 22.8%; Pred. No. 1.4e-08;
Matches 79; Conservative 58; Mismatches 160; Indels 49; Gaps 10;

QY 2 CGSGSGSSSTPNHPKVLVPTKQNNLQAOVPOAQNAPQAOAQNAPQAOV 61
DB 23 CGSGSAGNADRVBEK-----AQPV-----QSNSEPPSSAPIKNTNTATNDSLHD 67

QY 62 NAPOAQNAPQAOVAPQAEVTPVPOQOSQKIDGDF-----DKIGSVKLNKEAQTLESL 114
DB 68 KLSMSSSHDTSKENSQSSQSFAPLEQKQPAQENLTWTGVHSEVGNVNNVDKNDVTV- 126

QY 115 RFTLV---DKLGTBPKDKVSGKKIIEBKFLVNLSDINAEOLSGDFLIRSDDLFYGY 171
DB 127 -FTFVKYNSQVNDPVPDKTKTQS-----KTLISLVGKNENKEDYNTFLKDALF--- 175

QY 172 YHDTNGKLVDAADKFSQYFVYDEKRVNDSKLTATYRKKEGVYGSNPHTKFAAR 231
DB 176 YGSGYQPSADYKKVKYNYIYAKPDALNNENLALATATYQEDGYFVSVLSDVNRVGE 235

QY 232 -ISKLGDEIYFENGQAGSGSKDEKGNABFTTKGTQKLEITPTESNRRIIAILDQNG 290

Db 236 YIPOYGNVTLTFENGKIYGEIYRYNRRDDLFLQSLGEGQNLITPHK-----DNPH 286

QY 291 KYTTPQMEKAIMETFKIDSKAGNSDKYLIKEAKSDNQWQAIMVSEK 336
DB 287 KLSPTGPDNNAMELAFIN--AEKTDKKYVGVGKAETKYGLLFAEK 330

RESULT 3
US-10-696-544-12
; Sequence 12, Application US/10696544
; Publication No. US20040156865A1
; GENERAL INFORMATION:
; APPLICANT: Confer, Anthony W
; APPLICANT: Aralew, Sahlu
; APPLICANT: Murphy, George
; APPLICANT: Pandher, Karamjeet
; TITLE OF INVENTION: M. Haemolytica Outer Membrane Protein PlpE as a Vaccine or
; FILE REFERENCE: 03300-57188/02-744
; CURRENT APPLICATION NUMBER: US/10/696,544
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/422,305
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Mannheimia haemolytica
US-10-696-544-12

Query Match 12.6%; Score 219; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 QNASQAQNAPOAQNAPQAOVAPQAOVAPQAOVAPQAOVAPQAOVAPQAE 79
DB 1 QNASQAQNAPOAQNAPQAOVAPQAOVAPQAOVAPQAOVAPQAOVAPQAE 43

RESULT 4
US-09-797-385-10
; Sequence 10, Application US/09797385
; Publication No. US20020058042A1
; GENERAL INFORMATION:
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Blake, Milan S.
; TITLE OF INVENTION: Non-IGA Fc Binding Forms of the Group B
; Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/797,385
; FILING DATE: 01-Mar-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/923,992
; FILING DATE: 05-SEP-1997
; APPLICATION NUMBER: US 60/024,707
; FILING DATE: (vii)
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.


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; SEQ ID NO 72
; LENGTH: 3164
; TYPE: PRT
; ORGANISM: Herpes Virus
US-10-669-161-72

Query Match      8.1%; Score 141; DB 17; Length 3164;
Best Local Similarity 36.9%; Pred. No. 0.36;
Matches 41; Conservative 5; Mismatches 18; Gaps 3;

QY 2 GGSGGGS-SSTNHPKPVLPVKT-----QNNLQAGNVPOAQNASQAQN 44
DB 2872 GGVAPGGVSRRTTRQPVATPTTSARPRGHLTVSRLSAPOFQPOQPOFQPOQ 2931
QY 45 APOAQNAPOAQNAPOVENAPOAQNAPOVENAPOAEVTP-PVPOQSQKIDG 94
DB 2932 QPQFQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQNG 2982

RESULT 10
US-09-748-875-68
; Sequence 68, Application US/09748875
; Publication No. US20010016200A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/748,875
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: 09/298,523
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-68

Query Match      8.1%; Score 140.5; DB 9; Length 730;
Best Local Similarity 35.8%; Pred. No. 0.056;
Matches 29; Conservative 16; Mismatches 35; Indels 1; Gaps 1;

QY 13 PNHKPVLPVKTQNNLQAGNVPOAQNASQAQNAPQNAPOAQNAPOVENAPOAQNAPOV 72
DB 594 PEAPKSPVPEVPEAPKAPDTPQVPEAPKSPVPEVPEVPEVPEVPEVPEVPEVPEV 653
QY 73 ENAPOAEVTPVPQO-POSOKI 92
DB 654 PEAPKAPDTPQVPEAPKSPV 674

RESULT 11
US-09-298-523B-68
; Sequence 68, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-298-523B-68

Query Match      8.1%; Score 140.5; DB 10; Length 730;

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Best Local Similarity 35.8%; Pred. No. 0.056;
Matches 29; Conservative 16; Mismatches 35; Indels 1; Gaps 1;

QY 13 PNHKPVLPVPTONNLOAQNVPOAQNASQAQNAPOAQNAPOVNAPOAQNAPOV 72
Db 594 PEAPKSPVVKVPEAPKAPDTQVPEAPKSPVVKVSDTPKAPDTQVPEAPKSPVVKV 653

QY 73 ENAPOAEVTPPVQ-POSQKI 92
Db 654 PEAPKAPDTQVPEAPKSPV 674

RESULT 12
US-10-425-115-288440
; Sequence 288440, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 288440
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26148C.1.pap
US-10-425-115-288440

Query Match 7.9%; Score 137.5; DB 17; Length 756;
Best Local Similarity 23.4%; Pred. No. 0.099;
Matches 86; Conservative 40; Mismatches 130; Indels 111; Gaps 18;

QY 16 PKPVLVPTONNLOAQNVPOAQNASQAQNAPOAQNAPOAQ-NAPOVNAPOAQNAPOV 74
Db 429 PAP-----TKTAAAKTPAKAKTGAET--EATEAPAPVVEAGPSAPIAAKPALEE 481

QY 75 APQAEVTPPVQPOS--QKIDGSPDKIGSVKLNK-----AQTLERSFTLIVDKLGT 124
Db 482 KSSGHIAPEPTAPEALLETIDYIFRHASGKKLSEDEIAEARHYAQKLKYPKGLV----- 536

QY 125 PKPKDKVSGKKIIEKDFLV-----NLS-----DINAEQLSGDFLIRSDDLFVGY 172
Db 537 ---FNRSN-----EYDFLYLVPDNKLSVCREIGRIGFPKLEDDGLLILSKDDLADNLA 587

QY 173 HDTGKNLVDAAD-----KFSQVYVYDEKRVNDN--SDKLTATYRKKEGFVYGSNP 223
Db 588 Y--NGMKLAENKENCALAEANREISEWYQNLKRVSE-----LWQKERCPEKSLD 637

QY 224 HTKEFAARISKLG--DVEIKFENGQAQGS---IKDEKDGNAETFTIKGDTKQLEITPTES 278
Db 638 CVKIKAFKAFKVGAYSAAENFIQDPEGVVWEINGEATFEELISDRGD----- 686

QY 279 NRITIAILDQKQSYTRQMEKAIMETKFDISKAGNSQKYLIGBAKSDNW-----Q 329
Db 687 ---VCARSDDTK---DFSAEAILMGGRFY-----NDIWNQGREWAHE 723

QY 330 AIMVSEK 336
Db 724 IIMSEK 730

RESULT 13
US-10-767-701-56462
; Sequence 56462, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 56462
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30943377.pap
US-10-767-701-56462

Query Match 7.8%; Score 135; DB 16; Length 94;
Best Local Similarity 46.3%; Pred. No. 0.0095;
Matches 31; Conservative 7; Mismatches 23; Indels 6; Gaps 3;

QY 19 VLVPTQNNLQNVPOAQNASQAQNAPOAQNAPOAQNAPOVNAPOAQNAPOVNAPOA 78
Db 7 IVAPEQQPNVQ----PQSQQ-PQTQNPQNAQNPQGGQQPQVQ--PQVQQQPPVQQQPV 60

QY 79 EVTPPV 85
Db 61 SSTTNEP 67

RESULT 14
US-10-156-761-9880
; Sequence 9880, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9880
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9880

Query Match 7.6%; Score 132.5; DB 14; Length 447;
Best Local Similarity 28.6%; Pred. No. 0.12;
Matches 34; Conservative 9; Mismatches 41; Indels 35; Gaps 1;

QY 2 GSGSGSGSSSTPNHPKP-----VLVPKTON 26
Db 15 GGGPGGSGSSTPGTDPSSASACSASTPSTSGTSSPSGASSPSGTSSTSTS 74

QY 27 NLQNVPOAQNASQAQNAPOAQNAPOAQNAPOVNAPOAQNAPOVNAPOAEVTPPV 85
Db 75 STSAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAP 133

RESULT 15
US-10-739-930-10816
; Sequence 10816, Application US/10739930
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Query Match	7.4%;	Score 129;	DB 16;	Length 409;
Best Local Similarity	20.8%;	Pred. No. 0.19;		
Matches	73;	Conservative 57;	Mismatches 123;	Indels 98; Gaps 15;
Qy	4	SGSGSGSSSTENHFKPVLVPKTNLQAOQVFPQAOQNASQAQNAPOAQNAPOAQNAPOQVENA	63	
Db	14	SGAGSSSDAS-----VVPSEGSQSSGTTTP-----ASKQPOAQTAAPATASSTSSS	61	
Qy	64	POAQNAPO-----VENAPOA-----EVTTPVPVPOSQKIDG-SPDKIGSVKLN-----	105	
Db	62	SSDGKAPQAAATISTSTPFAAGTSNSNQVVTGTAEPQTMDEVRYTVDKENS-KLNTKGDG	120	
Qy	106	-----KEAQTLELSRFTLVLDKLGTPPKPKVSGKKIIIEEKQPLVL	145	
Db	121	KPKNRSSVDKDTKLIRNEDGKQDIVDTVTVTKTNEGDTIVTVTKPKQIDEGAD--VM	178	
Qy	146	NLSDINAEQLSGPFLIRRSDDLFGYGYHDTNGKNLVDAADKFQYFVYDEKRVN--DNI	203	
Db	179	ALLDYSKMGSEDDF-----NNAKDKIKLVTTLTSKANGQONL	217	

Qy 204 SD-----KLTATYRKKEGVGNSPHTKTEFAARISKLGIVETKFENG-----QAQGSIKDEK 255
 Db 218 NNRNTVELMTFYRKISDPIDLSGKTSBEVEBELNKIWD-KVKTQDWDGVDLQGAHKAR 276
 Qy 256 DGNAEFTIIGDTKOLSEITTPESNRITIAILDQNKSYTPGMEKAIMETKF 306
 Db 277 D-----TFKXESKK-----RQHVLSQGESITFSYELHNSVKEDKY 314

RESULT 17
 US-10-244-596-14
 ; Sequence 14, Application US/10244596
 ; Publication No. US2004005238A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hseu, Ruey-Shyang
 ; APPLICANT: Huang, Ya-Hui
 ; TITLE OF INVENTION: No. US2004005338A1el recombinant xylanases derived from anaerobic
 ; TITLE OF INVENTION: relevant sequences, expression vectors and hosts
 ; FILE REFERENCE: P22617
 ; CURRENT APPLICATION NUMBER: US/10/244,596
 ; CURRENT FILING DATE: 2002-09-17
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Neocallimastix patriciarum
 US-10-244-596-14

Query Match 7.3%; Score 127; DB 15; Length 448;
 Best Local Similarity 36.8%; Pred. No. 0.31;
 Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4;

Qy 2 GGSGSGSSSTPNHPKPLVLPKTNLLQAVPQAGNASQAQNAPOAQNAPQAQNAPOVE 61
 Db 240 GGAPAGGAPAGNDQPGQ---PQQQPPGQGPFPQQGQPPGQPPGQ-NDQGGQ 295
 Qy 62 NAPAQNAQPVENAPQAEVTPFPVQ-PQSXKIDGS 95
 Db 296 QPPQGPFPQNDQGGQ-QPPQGPQGGNPGGS 329

RESULT 18
 US-10-282-122A-64159
 ; Sequence 64159, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09

QY 123 GTPPKFDKVGSKKIIIEKDFVLNLSIDINAEOLSGDFLIRRDLLFYGYHDTNGKIL-V 181
Db 373 --IPSG-----EADYLLIDNYPILPESGDFISSK-----HHEVGGRKVKY 413
QY 182 DAADK---FSQVPVYDEKRVNDISDK-----LTIATYRKKEGFGVGSNPHYKFAARIS 233
Db 414 EACCKNLGVYFGMYEDENKKNETDKERKQTTSIKTYQFLGLRTPSE-----IP 469
QY 234 KLGDVBIKFGQAQGSIKDEKGNAEIETIKGDTKOLEITTESNRIIILIDONOKSY 293
Db 470 KGNVYTR---GSWFGYIGDDKTS-----YSATGDKKQDKNAEFN-----ADFNKKL 516
QY 294 TPMKEMKAIMETKPIDSKA---GNSDKYLIIBAKSDNW 328
Db 517 TGTSKRHDNQNPVENIKATFQNGRDNFE---GTATAENF 552

RESULT 21

US-10-282-122A-63567
; Sequence 63567, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

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; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

Db 317 PKPVV-----DLKQRIEPIESKPEVIKHIPOVEVQPKAQMVEPIEKPETKYIPQV 370
QY 73 ENAPQAEV-----TPPVPOQOSKIDGSDFKIGSVKLNKEAQTLELSRFTLVDK 121
Db 371 ESTQVEVHMKPVKTEYQOQLPIS-----GLQIKVPSAALQSK 415
QY 122 LGT---PPKFDKVGSKKI---IEEKDFVLNLSIDINAEOLSGDFLIIRSDDL-----F 168
Db 416 LDTGFQPROVERTTDSITVSVSHASLEKINALNHRIMSDIALKSDNTIKSSNFSRF 475
QY 169 Y-----CYHDTNGKILVDAADKFSQVYVYDEKRVND-----NISDKLTA 209
Db 476 YPENYVATKYSDPLYSDTN-QSL--TSDRFLDFTYTPKSRVNNYTPLRSTNFQNNAIS 532
QY 210 TYR 212
Db 533 NYR 535

RESULT 22

US-10-807-746-14

; Sequence 14, Application US/10807746

; Publication No. US20040219585A1

; GENERAL INFORMATION:

; APPLICANT: BAKALETZ, et al.

; TITLE OF INVENTION: NONTYPEABLE HAEMOPHILUS INFLUENZAE VIRULENCE FACTORS

; FILE REFERENCE: 28335/39196A

; CURRENT APPLICATION NUMBER: US/10/807,746

; CURRENT FILING DATE: 2004-03-24

; PRIOR APPLICATION NUMBER: US 60/458,234

; PRIOR FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 14

; LENGTH: 1013

; TYPE: PRT

; ORGANISM: H. influenzae

US-10-807-746-14

Query Match 7.0%; Score 121.5; DB 17; Length 1013;

Best Local Similarity 22.2%; Pred. No. 2.4;

Matches 78; Conservative 62; Mismatches 137; Indels 75; Gaps 16;

QY 27 NLQACNVPOACNQAQNAPOACNAPQVENAPOACNAPQVENAPOACNAPQVENAPOACNAPQVENA 86
Db 7 SLLACSTAFALNASTAY-AAQPTNQPTNQPTNQPTNQPTNQPTNQPTNQPTNQPTNQPTNQPTNQPTNQ 65
QY 87 PQSQKIDGSDFKIGSVKLNKEAQTLELSRFTL-----VDKLGTPPKFDKVGSKKIIE---- 138
Db 66 LEQINVSGSTENSCKTPPKIAETVKTAK-TLREQANNIKDIVKYE--TGVTVVEAGR 122
QY 139 -----EKDFVLNLSDI-NAEOLSGDFLIIRSDDLFYGY----- 171
Db 123 QSGGFAIRGVNDENRVAINIDGLRQAEITLSS-----QGKELFEGYGNFNTNGAEITLK 178
QY 172 -YHDTNGKILVDAADKFSQVYVYDEKRVNDNISDK-LTATYRKKEGFGVGSNPF--HTKE 227
Db 179 EVNITKGANSIKSGSGISGSGISGSGISGSGISGSGISGSGISGSGISGSGISGSGISGSGISGSG 236
QY 228 FAARISK-----LGDVEIKFENGQAQGSIKDEKQNAEIIKIGTKQLEI 273
Db 237 LAGRYKKFVILVVTTSRNGHELENYGKYNNDKIQGRREK----ADPYKIEQDSTLLKL 292
QY 274 T--PTESNRIIA--ILDQOK---SVTPGMEKAIMETKPIDSKAGSDCK 317
Db 293 SFNPTENHRFTLAADLVEHRSRGQDLSYTLKYLTPDLPEVDSRHTNDKTK 344

RESULT 23

US-10-425-115-281769

; Sequence 281769, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

Query Match 7.0%; Score 122; DB 15; Length 599;
Best Local Similarity 22.2%; Pred. No. 1.1;
Matches 54; Conservative 44; Mismatches 75; Indels 70; Gaps 13;

QY 16 PKPVLVPTKQTNLQANV-POAQNASQA-QNAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQ 72

APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12967
LENGTH: 2478
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12967

Query Match 6.7%; Score 117; DB 9; Length 2478;
Best Local Similarity 20.6%; Pred. No. 17;
Matches 83; Conservative 43; Mismatches 145; Indels 132; Gaps 16;

QY 26 NNQANVPO-----AQNAAQNAPOAQN--APQANAPQ-----59
DB 983 NOVQAATTKSDAKAEIAKASERKTAIEAMNDSTTEEQAAKDKVDQAVVTANADIDNA 1042
QY 60 -----VENAPQANQVENAPQAEVTPPVPOQSQKIDGSPKI---GSVKLNKEA-- 108
DB 1043 AANDVDNAKTNEATIAITPDANVPAKQAIADKVAQAEATIDGNNGSTTEKAAAK 1102
QY 109 ---QTLERSFTLVLDKLT-----PPKFDKVGSKKII-----BEKDF 142
DB 1103 QVQTEKTTADAIDAHTNAEVEAAKAAIAKIEAIQPATTTKDNAXEAIATKANERKT 1162
QY 143 LVNLSDINAEQLSG-----DFLIRSDDLFYGYHDTNGKNLVDAADKFSQYFVYVDEK 197
DB 1163 AIAQTQDITAEIAANADVNDNAVTOAN---SNIEAANSQNDVDQA-----K 1206
QY 198 RVNDNISDKLTATYRKKEGVYGSNPHTEKFAARISKL-----GDVEIKFEN 244
DB 1207 TTGENSIDQVTPVNNK---ATARNEITALLNNKLOEIQATPDATDEEQAAAEANTEN 1263
QY 245 GQAGSGIK-----DEKGNAEIP-----TIKGTQKLEBITPTESNRIT 284
DB 1264 GKANAISAATTNAQVDEAKANAEEAINAVTPKVKKQAAKDEIDQLQATQTN----- 1316
QY 285 ILQONOKSYTPGKEKATMETKFDISKAGNSDQKYLIGEAKSDN 327
DB 1317 VINNDQNAVTEKEAIIQQL-----ATAVTDKKNITATDDN 1354

RESULT 38
US-09-882-227-138
Sequence 138, Application US/09882227
Publication No US20030158396A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal

APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
FILE REFERENCE: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138
LENGTH: 298
TYPE: PRT
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: VARIANT
LOCATION: 12
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-882-227-138

Query Match 5.7%; Score 116.5; DB 10; Length 298;
Best Local Similarity 23.9%; Pred. No. 1.1;
Matches 59; Conservative 45; Mismatches 86; Indels 57; Gaps 12;

QY 79 EVTPFVP-----QPSQKIDGSDFKIGSVKLNKEAQT-----LELSRFTLVD----- 120
DB 32 QITIPPLEIQEIVKILDAFTL-NTELNTLAKRKQVYEQNNMLLDFNDINQNHKD 90
QY 121 -KLGTPPK-----FDKVGKKIIEEKFLVNLSDINAEQLSGDFLIERS 164
DB 91 AKITYPKRLKTLTLAPKGVFERKLG--EVCESTNKKTKLISEVSEVKMGYPVINS 148
QY 165 DDLFVGYVHDN--GKNLVDA--DKFSQYFVYDEKRVNDNISDKLTATYRKKEGVYVGS 221
DB 149 GRDLYGYVHDNNGENITIASRGEYAGFINYFEK-----PFAGGLCYPKVKD-----T 199
QY 222 NPHTKEFAARISKLDGVEIKFENGQAQSGSKDEKGNABEITIKGTQKLEBITPTESNRI 281
DB 200 NELLTKFLYFLYKLTNEIQI-MENLVFRGSI PALNKADIETLTI-----PIPLEIQQE 251
QY 282 IIAILDQ 288
DB 252 IVKILDQ 258

RESULT 39
US-10-702-305A-18
Sequence 18, Application US/10702305A
Publication No. US20040213803A1
GENERAL INFORMATION:
APPLICANT: Michael C. Chen
APPLICANT: Chuang-Jiun Chiu
APPLICANT: Zhong-Sheng Chen
APPLICANT: Dong-Sheng Chen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING OR
PREVENTING PNEUMOCOCCAL INFECTION
FILE REFERENCE: 12844-002001
CURRENT APPLICATION NUMBER: US/10/702,305A
CURRENT FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: US 60/424,497
PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 459
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence
US-10-702-305A-18

```

Query Match      6.7%; Score 116.5; DB 17; Length 459;
Best Local Similarity 22.8%; Pred. No. 2;
Matches 78; Conservative 56; Mismatches 131; Indels 77; Gaps 18;

QY      25 QNNLQ-AQNVPQAQNA--SQQAQFQ-AQNAQAQNAQVQENAPQAQNAQVQENAPQAE 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      83 QSNRQISENERKKQLAETDKETENAKQNLQKQEFNKVRAEIVPEAKGLAVTQK--KAE 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      80 VTTPVPQSQKIDGSFDFKIGSVKLNKQAOTLELSRF-----TL-----VDKL-- 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      141 EAKKEAEVAKRKYDVATLKVALAKEVEAKELEIEKLOQVEISTLEQEVATIAQHQVDNLKK 200
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      123 ---GTPPFKDYCKSKKIIIEKDFVLNLSLDINAQLSGDFLIRSDDLFCYGYHDTNGKN 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      201 LLAGADPD----DGTQVLEAK--LNKGAELNAKQAE--LAKQTQL-----EK 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      180 LVDAADKFSQYFVWVDEKRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARISKLGQVE 239
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      242 LLDLSDPEKQTQDELDKAAEAELDKADELQNKVADLEKGIAPVQIKVA-----E 292
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      240 IKFENGQAQGSIKQSKDGNAEFTTKG-----DTKQLSEITPTESNRIIIAILDONQKSYT 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      293 LNKETARLQSLDKDAEENNVDEYIKEGLEQATADKKAEELATTQKN-----IDTKQKD-- 344
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      295 PCWEKALMETK---FIDSKAGNSDQKYLIGEAKSD-NWQAI 331
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      345 --LEDAELELEKVLATLDPGEKQTQDE--LDKEAAEDANIEAL 382
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 40
US-10-437-963-185221
; Sequence 185221, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yengwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbezuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 185221
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MET4530_82138C.1.pep
US-10-437-963-185221

```

Qy	141	DFVLNLSGDIINAQLSGDFLRRSDLLFYGYHDTNGNLVDAADKFSQYVYVYDEKYN	200
Db	563	QFDVL-VGKIKLEGARDEVANAATPLVQAMFYNNGPSRFDAL	614
Qy	201	DNISDKLATATYK--KEGFVYGSN--PHTKEFAARISKLGDEIKFENGQAQGSIKDEX	255
Db	615	PD-----TYPKNKEAGSGASLALAMTKSLYTKI-----DI-----DAV	649
Qy	256	DGNABIFITKGTQLEITPTESNRILIAILDQNKQK---YFGMEKAIMETFIDSKAG	312
Db	650	DGFAD-----RTSEVALDLINDAQAADKIAGVDVDFQDTDLRTFTSG	694
Qy	313	NSD 315	
Db	695	NSD 697	

Search completed: December 17, 2004, 16:17:59
Job time : 178.595 secs

Db 829 TPTPKIPPELPQADPTQADPTPHVPSKAPAPRVPSPKTPEAPHVPSKAPAPR 888
QY 72 VENAPQAEVTPVPQ---PQSQKIDGSPDKIGSVKLNKEAQTLSRFTLVKLGTPPK 127
Db 889 VPESKTPPEAPHVPSKTPPEAKIP-----KPPKTPDVPKLPDVPLDVPK 936
QY 128 -----FDKVGSK---KIIEEK---DFLVNLNSDINAEQLSGDFLIIRS 164
Db 937 LPDAPKLPGLNKVQAVFTSTGNTKVTWFDKPTDADKHLKEVTTKELADKIA---- 992
QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVD-----EKRVDNNSDKLTATYRKKEG 216
Db 993 -----HKTGGTV-----RVFDLSLKGKETHVNGERTVRLALGQTGSDV 1033
QY 217 FVYGSNPHKFAARISKLGDE---IKFENGAQGSIKDEKGNABIFTIKGDTKQLEI 273
Db 1034 HVY---HVKE-----NGDLERIPSKVNGQV-----FKTNHFLFAIKTSLKDNQV 1077
QY 274 TPTESNRIIILDQNKSTPGMEKAIMET---KFIDSKAGN 313
Db 1078 TTPKQT-----KPSTQSQVEIAESQTGKF-QSKAAN 1108

RESULT 4
US-08-242-932-2
; Sequence 2, Application US/08242932
; Patent No. 5595740
; GENERAL INFORMATION:
; APPLICANT: Brady, L. Jeannine
; TITLE OF INVENTION: Cloning of No. 5595740-Iga Fc Binding Forms of
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,932
; FILING DATE: 16-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-242-932-2

Query Match 10.0%; Score 173; DB 1; Length 984;
Best Local Similarity 23.3%; Pred. No. 6.8e-07;
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;
QY 12 TPNHPEKVLVPTKQNNLQAVQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
Db 649 TPTPKIPPELPQADPTQADPTPHVPSKAPAPRVPSPKTPEAPHVPSKAPAPR 708
QY 72 VENAPQAEVTPVPQ---PQSQKIDGSPDKIGSVKLNKEAQTLSRFTLVKLGTPPK 127

Db 709 VPESKTPPEAPHVPSKTPPEAKIP-----EPPKTPDVPLDVPLDVPLDVPK 756
QY 128 -----FDKVGSK---KIIEEK---DFLVNLNSDINAEQLSGDFLIIRS 164
Db 757 LPDAPKLPGLNKVQAVFTSTGNTKVTWFDKPTDADKHLKEVTTKELADKIA---- 812
QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVD-----EKRVDNNSDKLTATYRKKEG 216
Db 813 -----HKTGGTV-----RVFDLSLKGKETHVNGERTVRLALGQTGSDV 853
QY 217 FVYGSNPHKFAARISKLGDE---IKFENGAQGSIKDEKGNABIFTIKGDTKQLEI 273
Db 854 HVY---HVKE-----NGDLERIPSKVNGQV-----FKTNHFLFAIKTSLKDNQV 897
QY 274 TPTESNRIIILDQNKSTPGMEKAIMET---KFIDSKAGN 313
Db 898 TTPKQT-----KPSTQSQVEIAESQTGKF-QSKAAN 928

RESULT 5

US-08-714-481-2
; Sequence 2, Application US/08714481
; Patent No. 5766606
; GENERAL INFORMATION:
; APPLICANT: Brady, L. Jeannine
; TITLE OF INVENTION: Cloning of No. 5766606-Iga Fc Binding Forms of
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,481
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,932
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-714-481-2

Query Match 10.0%; Score 173; DB 1; Length 984;
Best Local Similarity 23.3%; Pred. No. 6.8e-07;
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;
QY 12 TPNHPEKVLVPTKQNNLQAVQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
Db 649 TPTPKIPPELPQADPTQADPTPHVPSKAPAPRVPSPKTPEAPHVPSKAPAPR 708
QY 72 VENAPQAEVTPVPQ---PQSQKIDGSPDKIGSVKLNKEAQTLSRFTLVKLGTPPK 127
Db 709 VPESKTPPEAPHVPSKTPPEAKIP-----EPPKTPDVPLDVPLDVPLDVPK 756

QY 128 -----FDKVSCK---KLIBEK---DFLVNLSDINAEOLSGDFLIRRS 164
DB 757 LPDAPKLPDGLNKVQAVFTSTGNTKVTVVFDKPTDADKLHLKEVTTKELADKIA-----812
QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVYD-----EKRVNDNISDKLTATYRKKEG 216
DB 813 -----HKTGGGT-----RVFDLSLSKGGKETHVNGERTVRLALQGTGSDV 853
QY 217 FVYGSNPHTEFAARISKLGDVE---IKFENGQAQGSIKDEKGNABEFTIKGDTKQLEI 273
DB 854 HVY-----HVKE-----NGDLERIPSKVNGQVV-----FKTNHFSFLFAIKTLSKDQNV 897
QY 274 TPTESNRILIIAILDQNKSYTPGMEKAIMET---KFIDSKAGN 313
DB 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928
RESULT 6
PCT-US95-06111-2
; Sequence 2, Application PC/TUS9506111
; GENERAL INFORMATION:
; APPLICANT: Street address: 186 Grinter Hall
; APPLICANT: City: Gainesville Florida
; APPLICANT: State/Province: Florida
; APPLICANT: Country: US
; APPLICANT: Postal code/Zip: 32611
; APPLICANT: Phone number: 904-392-8929
; APPLICANT: Fax number: 904-392-6600
; APPLICANT: Telex number:
; TITLE OF INVENTION: Cloning of Non-IgA Fc Binding Forms of
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06111
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,932
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06111-2

Query Match 10.0%; Score 173; DB 5; Length 984;
Best Local Similarity 23.3%; Pred. No. 6.8e-07;
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHPKPVLPKTNLQAVNQVPOAQNASQANAPQANAPQAVENAPQANAPQ 71

DB 649 TPDTFKIPELQAPDTPQAPDTPHVPESPKAPEAPRVPESEKTPAEHPVPSKPAEAPR 708
QY 72 VENAPQAEVTPVPO-----POSQIDGSFDKIGSVKLNKEAQOTLELSRFTLVDKLGTTPK 127
DB 709 VPESKTPAEAPHVPESPKTPAPKIP-----EPKTPDVPKLPDVPKLPDVPK 756
QY 128 -----FDKVSCK---KLIBEK---DFLVNLSDINAEOLSGDFLIRRS 164
DB 757 LPDAPKLPDGLNKVQAVFTSTGNTKVTVVFDKPTDADKLHLKEVTTKELADKIA-----812
QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVYD-----EKRVNDNISDKLTATYRKKEG 216
DB 813 -----HKTGGGT-----RVFDLSLSKGGKETHVNGERTVRLALQGTGSDV 853
QY 217 FVYGSNPHTEFAARISKLGDVE---IKFENGQAQGSIKDEKGNABEFTIKGDTKQLEI 273
DB 854 HVY-----HVKE-----NGDLERIPSKVNGQVV-----FKTNHFSFLFAIKTLSKDQNV 897
QY 274 TPTESNRILIIAILDQNKSYTPGMEKAIMET---KFIDSKAGN 313
DB 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928

RESULT 7

US-08-923-992A-6
; Sequence 6, Application US/08923992A
; Patent No. 6280738
; GENERAL INFORMATION:
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Blake, Milan S.
; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B
; TITLE OF INVENTION: Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,992A
; FILING DATE: 05-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,707
; FILING DATE: 06-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-923-992A-6

Query Match 10.0%; Score 173; DB 3; Length 1128;
Best Local Similarity 23.3%; Pred. No. 8.3e-07;
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHPKPVLPKTNLQAVNQVPOAQNASQANAPQANAPQAVENAPQANAPQ 71

Db 793 TPDTKPIPELPQADPTDPHVPESKAPAPRVPSKTPPEAPHVPSKAPAPR 852
Qy 72 VENAPQAEVTPPVQ-----PQSKIDGDFDKIGSVKLNKEAQTLELSRFTLVKLGTPPK 127
Db 853 VPESKTPPEAPHVPSKTPPEAPKIP-----EPKTPDVPKLPDVKLPDVPK 900
Qy 128 -----FDKVSCK--KIIEK--DFLVNLSDINAEOLSGDFLIRRS 164
Db 901 LPDAPKLPGLNKGAVFTSTGNTKVTVDKPTDADKLHLKEVTTKELADKTA----- 956
Qy 165 DDLFYGYHDINGKLVDAADKFSQYFVVD-----EKRVDNDSKLTATYRKKEG 216
Db 957 -----HKTGGGV-----RVFDSLKSGKGKETHVNGERTVRLALGQTGSDV 997
Qy 217 FVYGSNPHYKFAARISKLGDE--IKFENGQAQGSIKDEKGNABEFTIKGDTKOLEI 273
Db 998 HVY-----HVKE-----NGDLERIPSKVGVV-----FKTNHPSLFAIKTSLKQNV 1041
Qy 274 TPESNRITIIILDONQKSYTPGMEKAIMET---KFDISKAGN 313
Db 1042 TPKQT-----KPTQSGQVEIAESQTGKF-QSKAAN 1072

RESULT 8
US-08-923-992A-8
; Sequence 8, Application US/08923992A
; Patent No. 6280738
; GENERAL INFORMATION:
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Blake, Milan S.
; TITLE OF INVENTION: No. 6280738-IGA Pc Binding Forms of the Group B
; TITLE OF INVENTION: Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,992A
; FILING DATE: 05-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,707
; FILING DATE: 06-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2500
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1098 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-923-992A-8

Query Match 9.7%; Score 168; DB 3; Length 1098;
Best Local Similarity 23.0%; Pred. No. 2.3e-06;
Matches 79; Conservative 45; Mismatches 115; Indels 104; Gaps 15;
Qy 12 TPNHKPVLPVKTQNNLQNVQVQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71

Db 792 TPDTKPIPELPQADPTDPHVPESKAPAPRVPSKTPPEAPHVPSKAPAPR 851
Qy 72 VENAPQAEVTPPVQ-----PQSKIDGDFDKIGSVKLNKEAQTLELSRFTLVKLGTPPK 127
Db 852 VPESKTPPEAPHVPSKTPPEAPKIP-----EPKTPDVPKLPDVKLPDVPK 899
Qy 128 -----FDKVSCK--KIIEK--DFLVNLSDINAEOLSGDFLIRRS 164
Db 900 LPDAPKLPGLNKGAVFTSTGNTKVTVDKPTDADKLHLKEVTTKELADKTA----- 955
Qy 165 DDLFYGYHDINGKLVDAADKFSQYFVVD-----EKRVDNDSKLTATYRKKEG 216
Db 956 -----HKTGGGV-----RVFDSLKSGKGKETHVNGERTVRLALGQTGSDV 996
Qy 217 FVYGSNPHYKFAARISKLGDE--IKFENGQAQGSIKDEKGNABEFTIKGDTKOLEI 273
Db 997 HVY-----HVKE-----NGDLERIPSKVGVV-----FKTNHPSLFAIKTSLKQNV 1040
Qy 274 TPESNRITIIILDONQKSYTPGMEKAIMET---KFDISKAGN 313
Db 1041 TPKQT-----KPTQSGQVEIAESQTGKF-QTKAAN 1071

RESULT 9
US-08-515-251A-2
; Sequence 2, Application US/08515251A
; Patent No. 5891677
; GENERAL INFORMATION:
; APPLICANT: GERLACH, GERALD F.
; APPLICANT: WILLSON, PHILIP J.
; APPLICANT: ROSSI-CAMPOS, AMALIA
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: ACTINOBACILLUS PLEUROPEUMONTAE OUTER
; MEMBRANE LIPOPROTEIN A AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/515,251A
; FILING DATE: 15-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,558
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0027.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-515-251A-2

Query Match 9.2%; Score 159.5; DB 2; Length 365;
Best Local Similarity 24.1%; Pred. No. 2.7e-06;
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21;

QY 1 CGSGSGSSSTPNHPKFLVLPKTONNQVPOAQNASOQAPQAPQAN 56
Db 20 CGSGSGSSSSKPNSE--LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64
QY 57 -----APQVENAPQAN-----APQVENA-----PQAEVTPVPVPOQSQKIDGSPKIGSVK 103
Db 65 EPEKAPQVD-SPKAEPRNPAPGNPKLNDPQV-NAPKMDNPKQAPKGE-----E 115
QY 104 LNKEAQTELGRFTLVLDKL--GTPPKFKDKVSGKIIIEKFL--VLNLSIDINAEQLSGDF 159
Db 116 LSKDSKNAEILKELGVKDINGSINNADVLNLK-IDEKDHTVLDKGINRNLKVTN 174
QY 160 LIRRSDDLFGYHYHTGKNLVDAADKFSQY--FVYDEKRVNDNISDKLTATYRKKEGF 217
Db 175 TISAQDI-----KTLKSSGKLLGYGYMQLNQVRQDENYSDEKVS-----E 220
QY 218 VYGSNPHUKFAAR--ISKLGVEIKFE--NGOAGSIIKDEKGNAEIFTIK-----265
Db 221 LLSYNDADKIRPTKSIYKGMFYKYDVGNQKLKASVEASYDDVTYKVMKVGENDY 280
QY 266 -----GTLQLEIPTTES-----NRIIAILDQNKSYTPGMEKAIMETKFIDSK 310
Db 281 WKLGFGRTNLLENQVTGAKVGEDGTIINGTLYSKIDNFKLTP-----DANFSGGI 333
QY 311 AGNSDKYLLIGKSNHQAIM 332
Db 334 FKGNGE-VLAGSAISERKQWGI 354

RESULT 10
US-08-515-251A-4
; Sequence 4, Application US/08515251A
; Patent No. 5891677
; GENERAL INFORMATION:
; APPLICANT: GERLACH, GERALD F.
; APPLICANT: WILLSON, PHILIP J.
; APPLICANT: ROSSI-CAMPOS, AMALIA
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE OUTER
; TITLE OF INVENTION: MEMBRANE LIPOPROTEIN A AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/515,251A
; FILING DATE: 15-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,558
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0027.10
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-515-251A-4
Query Match 8.0%; Score 138.5; DB 2; Length 367;
Best Local Similarity 22.1%; Pred. No. 0.00022;
Matches 91; Conservative 61; Mismatches 105; Indels 155; Gaps 26;
QY 1 CGSGSGSSSTPNHPKFLVLPKTONNQVPOAQNASOQAPQAN-----APQAN 56
Db 20 CGSGSGSSSPKPNSES---TPKVDMSAPKAEQPKKEAPQA-DSPKAEKPKSIAPLWME 75
QY 57 APQVENAPQANAPQVENAPQA---EVTTP---VPQSQKIDGSPDK-----98
Db 76 NPKVEK--QRENVLQ-EKSPKADPEQVMDPKLGAQKDDQKLEEPKNSNAEILKELGK 132
QY 99 -----IGSVKLKNEAQTLSESRFTLV-----DKLGTTPPKFKDKVSGKIIIEKD---141
Db 133 DITSGTISISDIETELNQLDSNDNVKISLLNENLMRDNLIN---NKIAGSDIRTLKDSGG 189
QY 142 -----FLVLN-----LSDINAEQLSGDFLIRRSDDLFGYHYH 173
Db 190 RLLGYGYVQLNQVTQDSRDPDNYKHQFENHYLLSMNDAEKILPEKSLEYKSGMTYGY--247
QY 174 DTNGKVLVDAADKFSQYFVYDEKRVNDNISDKLTATYRKKEGFYVGSNPHUKFAARIS 233
Db 248 NTSG-----NEKLTAEVNAK-----YDSS--TKKLSMKVY 275
QY 234 -----KJGDV---BIKFENGAQSGSIKDEKDG--NAEFTIKGTQKLEITPTESNRII 282
Db 276 DNDRYWKLGEVMSNNVRLPEEKVDG-VKVDSDGTINARLYL--STEERPLKLT-----325
QY 283 IAILDQNKSYTPGMEKAIMETKFIDSKAGNSDQKYLIGEAKS--DNWQAIM 332
Db 326 ----DAN-----FSGG-----IFGKNG-----EVLAKGAESIKGEQWGI 356

RESULT 11
US-08-155-888-2
; Sequence 2, Application US/08155888
; Patent No. 6066623
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hedstrom, Richard C.
; APPLICANT: Sedegah, Martha
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE
; TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR
; TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: Bldg. 1, T-12 8901 Wisconsin Ave.
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,888
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spevack, A. David
; REGISTRATION NUMBER: 24,743
; REFERENCE/DOCKET NUMBER: N.C. 75,851
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 295-6759
; TELEFAX: (202) 295-1022
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```

Db      312 QPFGGQPPGGNDQQQG-QPPGPGGPNPGGS 345

RESULT 13
US-09-390-200-2
; Sequence 2, Application US/09390200
; Patent No. 6137032
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; TITLE OF INVENTION: Anaerobic Fungus
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/390,200
; APPLICATION NUMBER: US/09/390,200
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 493-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-390-200-2

Query Match          7.3%; Score 127; DB 3; Length 485;
Best Local Similarity 36.8%; Pred. No. 0.0038;
Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4

Qy    2   GGSGSSSTPNHPKVLVPTQTNNLQAQNVPAQNASOAQNAPQAQNAQVAQE 61
       |||::||::||::||::||::||::||::||::||::||::||::||::||:
Db    256  GGAFAGAPAGNDQFPQG---PFGQPDPGQPPGQPPGQPPGQPPGQ--NQDQGG 311
       |||::||::||::||::||::||::||::||::||::||::||::||::||:
Qy    62  NAPAQNAQPVENAPAEVTTPVFQ-POSQIDGS 95
       |||::||::||::||::||::||::||::||::||::||::||::||::||:
Db    312 QPFGGQPPGGNDQQQG-QPPGPGGPNPGGS 345

RESULT 14
US-08-487-890A-115
; Sequence 115, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony

```


DB 517 TGTSKRDHNPVFNKATFQNGRDNFE---GTATAENF 552

RESULT 16

US-08-337-483-115
; Sequence 115, Application US/08337483
; Patent No. 5922562
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-337-483-115

Query Match 7.2%; Score 124; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;
QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGFDKIGSVKLNKEAQTLELSRFTLVYDKL 122
DB 322 VFSAKETEERKPLPKETLIDGKLTFTSKTDTTNTKTSKNTTE-----NFTTKD-- 372
QY 123 GTPPKFDKVSCKKIEEKDFLVNLSDINAEQLSGDFLIIRSDDLFVGYVYHDTNGKNL-V 181
DB 373 --IPSEF-----EADYLLIDNVPILPLPESGDFISSK-----HHEVGGKRYKV 413
QY 182 DAADK---FSQYFVYDEKRVNDISDK-----LTATYRKKEGFVYGSNPHTKFAARIS 233
DB 414 EACCKNLVYKFGMYEDKENNKNETDKEKEKQTTTSIKTYQFLGLRTPSE-----IP 469
QY 234 KLGDEVEIKFNGAQSIGKDEKGNAEIFIKGDTKQLEITPTESNRIITAILDQNKSY 293
DB 470 KMGVNTYR---GSNFGYIGDKTS-----YSATGDKRQDKNAPAEFN-----ADFNNKKL 516
QY 294 TPGMEKAIMETKFTDSKA-----GNSDQKYLIGBAKSDNW 328
DB 517 TGTSKRDHNPVFNKATFQNGRDNFE---GTATAENF 552

RESULT 17

US-08-478-373-115
; Sequence 115, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-373-115

Query Match 7.2%; Score 124; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;
QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGFDKIGSVKLNKEAQTLELSRFTLVYDKL 122
DB 322 VFSAKETEERKPLPKETLIDGKLTFTSKTDTTNTKTSKNTTE-----NFTTKD-- 372
QY 123 GTPPKFDKVSCKKIEEKDFLVNLSDINAEQLSGDFLIIRSDDLFVGYVYHDTNGKNL-V 181
DB 373 --IPSEF-----EADYLLIDNVPILPLPESGDFISSK-----HHEVGGKRYKV 413
QY 182 DAADK---FSQYFVYDEKRVNDISDK-----LTATYRKKEGFVYGSNPHTKFAARIS 233
DB 414 EACCKNLVYKFGMYEDKENNKNETDKEKEKQTTTSIKTYQFLGLRTPSE-----IP 469

QY 234 KLGDEVEIKFENGQAGSISKDEKGNABFTIKGTQKLEITPTESNRILIIAILDONOKSY 293
DB 470 KMGNTYR---GSGWFGYIGDDKTS-----YSATGDKROKDNAPAEFN-----ADFNKKL 516

QY 294 TPGMEKAIMETKFIDSKA----GNSDOKYLIGEAKSDNW 328
DB 517 TGTSKRHDNQNPVFNKATFQNGRNDPE---GTATAENF 552

RESULT 18
US-08-474-671-115
; Sequence 115, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-465 MJS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-671-115

Query Match 7.28; Score 124; DB 3; Length 631;
Best Local Similarity 24.08; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPOAEVTPVPQPO-----SOKIDGSDFKIGSVKLNKEAQTLESEFTLVKDL 122
DB 322 VFSKTEEPKLPKRETLIDGKLTFTSKTDTTNTKTSKNTNTE-----NFTTKD-- 372

QY 123 GTPPKFDKVGKKIIEKDFLVNLSDINABQLSGDFLIRSDDDLFGYGYHDTWCKNL-V 181
DB 373 --IPSG-----EADYLLIDNYPILPLPESGDFISSK-----HHEVGGRYKV 413

QY 182 DAADK---FSQVYVYDEKRVNDNISDK-----LTATYRKEGEGFYVGSNPHTKFAARIS 233
DB 414 EACCKNLGVKFGMYVEDKENNKNETDKEKEKQTTSIKTYVQFLGLLTPSSE---IP 469

QY 234 KLGDEVEIKFENGQAGSISKDEKGNABFTIKGTQKLEITPTESNRILIIAILDONOKSY 293
DB 470 KMGNTYR---GSGWFGYIGDDKTS-----YSATGDKROKDNAPAEFN-----ADFNKKL 516

QY 294 TPGMEKAIMETKFIDSKA----GNSDOKYLIGEAKSDNW 328
DB 517 TGTSKRHDNQNPVFNKATFQNGRNDPE---GTATAENF 552

RESULT 19
US-08-483-577A-115
; Sequence 115, Application US/08483577A
; Patent No. 6015668
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-577A-115

```

Query Match          7.2%; Score 124; DB 3; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14

QY      72  VENAQAQVATPVPOQP-----SOKIDGGFDKIGSVKLKNEAQTLLEGRFTLVLDKL 122
DB      322 VPSAKETBEKPKLPKETLIDGKLITFSKTYDTTNTKTSIAKTYE-----NFTTKD-- 372
QY      123 GPPPKFDKVSCKKIEEKDFVLVNLSDINAEQLSGDFLIRRSDDLFGYHYHTDNGKLV 181
DB      373 --IPSFG-----EADYLLIDNYPILPLPSGDFPISSK-----HHEVGGKRYKV 413
QY      182 DAADK--FSQYFVVYDEKRVNDNISDK----LTATVRKKEGFVYGSNPHTKEFAARIS 233
DB      414 EACCKNLCTVFGMYIEDKKNKNETDKEKEKQTTTSIKYIYQFLGLRTPSE-----IP 469
QY      234 KLGDEIIEKFENGQAQGSIKDEKGNABIFIKGTQKLEITPTESNRILIALDQNKQSY 293
DB      470 KMGNVYR--GSWFGYIGDDKTS-----YSATGDKROQKNAPAEFN-----ADFNKKL 516
QY      294 TPGMEKATMEYKFDISKA-----GNSDQKYLIGEAKSDNW 328
DB      517 TGTSKRHNDQNPVFIKATFQNGRDNDFE--GTATAENF 552

RESULT 20
US-08-897-438-115
; Sequence 115, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pale
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1A7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-720
; TELECOMMUNICATION INFORMATION:

```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-654-115

Query Match          7.2%; Score 124; DB 3; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SQKIDGSPDKIGSVKLNKEAQTLELSRFTLVDKL 122
DB 322 VFSKETEELPKPKETLIDGKLTFTSKTTDTTNTKTSKNTTE-----NFTTKD-- 372
QY 123 GTPPKFDKVSCKIIEEKDFVLNLSINAQLSGDGLIRSDDLFYGYHDTNGKLV 181
DB 373 --IPSGF-----EADYLLIDNYPILPLPSGDFISSK-----HHEVGKRYKV 413
QY 182 DAADK---FSQYFVYDEKRVNDISK-----LTATYRKKEGFGVGSNPHTKFAARIS 233
DB 414 EACCKNLGVKFGMYEDKENNKETDKEKEKQTTTSIKTYQFLGLRTPSSE---IP 469
QY 234 KLGDFEIKFENGQAQGSIKDEKGNAEFTIKGTQKLEITPTESNRILIAILDQOKSY 293
DB 470 KMGNTVYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAFBN-----ADFNKKL 516
QY 294 TPGMEKAIMETKFDISKA---GNSDQKYLIGEAKSDNW 328
DB 517 TGTSKRHDNQNPVFNKATFQNGRNDPE---GTATAENF 552

RESULT 22
US-08-649-518-115
; Sequence 115, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: /US/08/649,518
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-649-518-115

Query Match          7.2%; Score 124; DB 3; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SQKIDGSPDKIGSVKLNKEAQTLELSRFTLVDKL 122
DB 322 VFSKETEELPKPKETLIDGKLTFTSKTTDTTNTKTSKNTTE-----NFTTKD-- 372
QY 123 GTPPKFDKVSCKIIEEKDFVLNLSINAQLSGDGLIRSDDLFYGYHDTNGKLV 181
DB 373 --IPSGF-----EADYLLIDNYPILPLPSGDFISSK-----HHEVGKRYKV 413
QY 182 DAADK---FSQYFVYDEKRVNDISK-----LTATYRKKEGFGVGSNPHTKFAARIS 233
DB 414 EACCKNLGVKFGMYEDKENNKETDKEKEKQTTTSIKTYQFLGLRTPSSE---IP 469
QY 234 KLGDFEIKFENGQAQGSIKDEKGNAEFTIKGTQKLEITPTESNRILIAILDQOKSY 293
DB 470 KMGNTVYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAFBN-----ADFNKKL 516
QY 294 TPGMEKAIMETKFDISKA---GNSDQKYLIGEAKSDNW 328
DB 517 TGTSKRHDNQNPVFNKATFQNGRNDPE---GTATAENF 552

RESULT 23
US-09-270-767-43054
; Sequence 43054, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 43054
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43054

Query Match          7.0%; Score 121; DB 4; Length 808;
Best Local Similarity 28.1%; Pred. No. 0.028;
Matches 56; Conservative 22; Mismatches 63; Indels 58; Gaps 12;

QY 15 HPK-----PVLVPKTONNLQONVP-----CAQNASQAQNAQ-----QAQNAQ 53
DB 307 HPQKQQTFFPAPQTPGTYVYRPIFVGEKSEPIINAHKEIPNQAPPSSAQQAQAY 366
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QY 54 AQAPOVENAQAPOVENA-POAEVTPPV-OPQSQKIDGSDFKIGSVKLNKE 107
 Db 367 AQAQFQVHAAPQOHNPPTLNTQPSQEQVVEGAAGLPPTPHILNSINKIQDI---Q 422
 QY 108 AOTLESLRRTLVDKLTGTPPKFVKVSGKKIIEKDFLVNLSDINAEQSLGDFLIRSDLL 167
 Db 423 RDVLEL-----MG---KVEQFKGTR--BEKEYALD-----EMLTRNL--KLPTI 461
 QY 168 FYGYHDTNGKNLVDAADK 186
 Db 462 -----DTNGKDSIRLARK 474

RESULT 24
 US-09-134-000C-6588
 ; Sequence 6588, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 6588
 ; LENGTH: 1308
 ; TYPE: PR1
 ; ORGANISM: Enterococcus faecalis
 ; US-09-134-000C-6588

Query Match 7.0%; Score 121; DB 4; Length 1308;
 Best Local Similarity 19.4%; Pred. No. 0.057;
 Matches 85; Conservative 59; Mismatches 157; Indels 138; Gaps 18;
 QY 3 GSGSGSSSTPNHPKPVLPKTONNLOAQNP-----QAQNASQON-APQQA 49
 Db 98 GIAEQSSATSDNTTNNQOPTAEAKSAQEQPVVSPETTIEPLGQPTVAPAEANDANKST 157
 QY 50 NAFQAQNAPOVENA-POAQAPOV-----ENAPQAEVTPPVPOSQXI 92
 Db 158 SIPKFEPTPDVKADEAKDPNITVVEKPTEDLGNVSSKDLAAKEVDQLOKEQAQKI 217
 QY 93 -----DGSFDKIGSV-----KLNKEAQTLELSRF----- 116
 Db 218 AQAALAKAKNEIAKENAEIAAKNAEKERYEKEVAEYNKHNDKGYVNEAISKDLVFD 277
 QY 117 -TLVDKLTGTPPKFVKVSGKKIIEKDFLVNLSDINAEQSLGDFLIRSDLLFYGYHDT 175
 Db 278 SSIVTK---DTKIDKITGGKFIKASDFNKNVQ-----QSKDIFTKLSKDM 320
 QY 176 NGK-----NLVDAADKFSQYFVYDEKRVNDNISDKLTATY--RK--KEGFVYGS 221
 Db 321 NGRATGNFQSSKYSVAVEFGPKGGVAVLEKKNPVNTYTG-LNASYLNKRITKABEYI-- 377
 QY 222 NPHTEFAARISKLGDEVEIKFENGQAQGSTKDEKGNAE-----IFTIK-GDTKQLEITPT 276
 Db 378 -----ELQSAFQSGTLLNVAFSNDPIITAFVGTKNAGKDKVRLTIKLYDANGKEVLPE 432
 QY 277 ESNRIITAILDQCKSYTPGMEKAIMETKFDISKAGNSDOKYLIGE----- 322
 Db 433 KDAFAFALSLSNS---SLGNTSVSEHAEFVSDFGSKNEFYKINGSVYKQADKKEYSTE 489
 QY 323 -----AKSDNQAI 331
 Db 490 DLDYGTGPGSLKNSDVAW 508

RESULT 25

US-08-750-152A-2
 ; Sequence 2, Application US/08750152A
 ; Patent No. 5977331
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAKURA, YOKO
 ; APPLICANT: KIMURA, EIICHIRO
 ; APPLICANT: ABE, CHIZU
 ; APPLICANT: KAWAHARA, YOSHIO
 ; APPLICANT: NAKAMATSU, TSUYOSHI
 ; TITLE OF INVENTION: ALPHA-KETOGLUTARATE DEHYDROGENASE GENE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22152
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/750,152A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NORMAN P. OBLON
 ; REGISTRATION NUMBER: 24,618
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1257 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-750-152A-2

Query Match 6.7%; Score 116.5; DB 2; Length 1257;
 Best Local Similarity 22.1%; Pred. No. 0.14;
 Matches 91; Conservative 54; Mismatches 121; Indels 145; Gaps 24;
 QY 7 GGSSTPNHPKPVLPKTONNLOAQNPQAQNASQONAPQQAPOAQAPOAQAPOAQA 66
 Db 76 GGNATP-----ATTEAQ--PSAPKES-AKPAKPA--APAKAAPRVETKPA 118
 QY 67 QNAPQVE--NAPQAEVTPPVPOSQKIDGSDFKIG-SVKLNKEAQTLE----- 111
 Db 119 KTAQAKKESVPO---QPKLPEQGTPIRGIFKSIKAKMDISLEIPTSVDMPARLMF 175
 QY 112 -----ELSR-----FTLVDKLTGTPP---KFDKVSQKIIIEKDFLVN 146
 Db 176 ENRAMVNDOLKTRGKISFTHIIGYAMVKAHMAHPDMNNSYDVIDGKPTLIVPEHINLG 235
 QY 147 LSDINAEQSLGDFLIRSDLLFYGYHDTNGKNLVDAADK-----FSQYFVYDEKRVN 200
 Db 236 LA-IDLPQKDG-----SRALVVAIKETKKNFSEFLAAY-EDIVT 274
 QY 201 DNISDKLTATYRKKEGFVYG-SNP---HTKEFAARISK-----LGDVEIKFENGQAQ 249
 Db 275 RSRGKLTWD--DYQGVTVSLTNFGGIGTRHSVRLTKGQGTIIGVSGMDYPAE---PQ 329
 QY 250 SIKDEKGNABEFTIKGDTKQLEITPTESNRIIA-----ILD 287
 Db 330 ASEDRL---AEL-----GVGKLVITITSTYDHRVIOGAVSGEFLRTMSRLLLTDSFWEIDF 382
 QY 288 QNQKSYTP-----GMEKAIMETKFDISKAGNSDQKYLIGEAQSDNW 328

Db 393 AMNVPYPMRWAQDPVNTGVKNTVRVQMLIAYBSRG---HLIADTNPWSW 430
Query Match 6.7%; Score 115.5; DB 4; Length 881;
Best Local Similarity 22.9%; Pred. No. 0.1;
Matches 66; Conservative 34; Mismatches 83; Indels 105; Gaps 14;

RESULT 26

US-09-486-072-2
; Sequence 2, Application US/09486072
; Patent No. 6489155
; GENERAL INFORMATION:
; APPLICANT: Masanori TAKAYAMA, et al.
; TITLE OF INVENTION: GENES
; FILE REFERENCE: 11202/1
; CURRENT APPLICATION NUMBER: US/09/486,072
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/JP98/02310
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: JP252624/97
; PRIOR FILING DATE: 1997-09-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 881
; TYPE: PRT
; ORGANISM: Bacteria
US-09-486-072-2

Query Match 6.7%; Score 115.5; DB 4; Length 881;
Best Local Similarity 22.9%; Pred. No. 0.1;
Matches 66; Conservative 34; Mismatches 83; Indels 105; Gaps 14;

QY 1 CGGSGSGSSSTPHPKPVLVPTQNNLQAVPQANASQANAPQANAPQAV 60
DB 18 CGGSGSEASS-----PEV-----EVDNGVEIQPEPEPEPEPEPEV 56
QY 61 ENAPQANAPQAVENAPQAVTPPV-POPO-----SOKIDGSDKGSVKLNK 106
DB 57 EPE 110
QY 107 EAQLELSRFTLVKLTGTPPKFKVSGKKIIEKDFLVNLSD-----INAEQL 155
DB 111 ESHVNEYQVAPAVEQIAAIP-----GLK-----WLQVNLNGAFGRFIVPVEVEAI 158
QY 156 SGDFLIRRSDDLFGYHYDINGKLVDA-----DKFSQYFVWYDEKRVNDSKLTATY 211
DB 159 NPSAPNSADLF-----DPALPGDDLFEQ-----IALGLQAKG 192
QY 212 RKKEGFVYGSNPHTKFAARISKLGDEVEIKFENGQAQGSINDEKQNA 259
DB 193 IKVAYIATQGFAMLKGAERS-----MDFD-----SIVDESQGA 229

RESULT 27

US-09-134-001C-5106
; Sequence 5106, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Decette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5106
; LENGTH: 1177
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5106

Query Match 6.7%; Score 115.5; DB 3; Length 1177;
Best Local Similarity 17.7%; Pred. No. 0.15;
Matches 68; Conservative 68; Mismatches 161; Indels 87; Gaps 14;

QY 25 QNNLQAVPQANASQANAPQANAPQANAPQANAPQANAPQANAPQAV 84
DB 248 EKNQCKQQTAAQTSSSENHNVKSNYQTTKRTNYSKVDNTININIASQIVBEI 307
QY 85 POPQSQKI--DGSFQKIGSVKLNKEAQTLERFLVDKL----- 122
DB 308 RRERKRVLQKRFRKALQQRQNNQSEEDSIQKAIDEMTAKQAQHTGESSLDLENES 367
QY 123 ---GTPPKFKVSGKKIIEKDFL-----VLNLSDNAEQLSGDFLI-----RRSDDL 168
DB 368 NQDSSNSLEKQSSNNDKNAQNTFLFNVEIEDLDTSDVYKVNBEETESKNDEDLV 427
QY 169 -YGYHYDINGKLVDAADKFSQYFVYDEKVN-----DNISDKLTATYRKKEGFVYGSN 222
DB 428 SSNHYHSNDAAVEDA-----EYHLDNROQNSQODDIISKSSSTNNYDNASVASV 482
QY 223 PHTKEFAARISKLGDEVEIKFENGQAQGSIKDEK-----DGNAEIETI-----K 265
DB 483 DNTERAKSNEDKNDTEITHLDTTSKVSDEKIESNTNHLQODKVKLVKNVSLKSSN 542
QY 266 GDTKOLE-----ITPESNRILAILDONOKSYT-PCM--EKAIMETKTFIDS 309
DB 543 SDTGTRKQRFQSGSRPFNVLMTPSDKKK-----MMDQNHKKVSPPELPEKQANANHRKDS 598
QY 310 KAGNSDOKVLIG---EAKSDNWOA 330
DB 599 ESNKEEFKQINTNRETOSNYES 622

RESULT 28

US-08-613-009A-10
; Sequence 10, Application US/08613009A
; Patent No. 6090576
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613.009A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-542
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-613-009A-10

Query Match
Best Local Similarity 6.6%; Score 114; DB 3; Length 682;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSGSSTPHKPKVLPVKTQNNLQAVPQACNAPQACNAPQACNAPQV 60
DB 1 CG-GSGGS-----NPPAPTPIP-----NAGSGTGTGAGGTDNTANA 39
QY 61 ENAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQV 120
DB 40 GNTGTNSGTGSANTPEPKY-QDVPTKEKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 93
QY 121 KLGTPPKFQKVSQKIIIEKDFVLNLSIDINAEQLSG--DFLIRSDDLFYGYHDTNGK 178
DB 94 RQDTP-----LDEKNIIITLGGKQVAGKKSPLPFLSDVENKLLDGYIAKMN-- 140
QY 179 NLVDAADKFSQYFVVYDE-KRVNDNISDKLTATYRKKEGFVYGSNPHTKPEFAARISKLD 237
DB 141 ----VADKNA-----IGDRIKKNKEISDEBELAKQIKE-----AVRKSHEFQOVLSSLEN 186
QY 273 ITPTESNRRIIAILDQKQSYTPGMEKAIMETKIDSKAGNSDKYLIKEAKSDNQWAIM 332
DB 245 ELPTQD-----AVKYKGHDFM--TDVANRRNRFSEVKE-NSQAGWYGYGASSKDEYNRL 296
QY 333 VSE 335
DB 297 TKE 299

RESULT 29
US-08-778-570B-12
Sequence 12, Application US/08778570B
Patent No. 6437096
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570B
FILING DATE: 03-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-664
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-778-570B-12

Query Match
Best Local Similarity 6.6%; Score 114; DB 4; Length 682;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSGSSTPHKPKVLPVKTQNNLQAVPQACNAPQACNAPQACNAPQV 60
DB 1 CG-GSGGS-----NPPAPTPIP-----NAGSGTGTGAGGTDNTANA 39
QY 61 ENAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQV 120
DB 40 GNTGTNSGTGSANTPEPKY-QDVPTKEKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 93
QY 121 KLGTPPKFQKVSQKIIIEKDFVLNLSIDINAEQLSG--DFLIRSDDLFYGYHDTNGK 178
DB 94 RQDTP-----LDEKNIIITLGGKQVAGKKSPLPFLSDVENKLLDGYIAKMN-- 140
QY 179 NLVDAADKFSQYFVVYDE-KRVNDNISDKLTATYRKKEGFVYGSNPHTKPEFAARISKLD 237
DB 141 ----VADKNA-----IGDRIKKNKEISDEBELAKQIKE-----AVRKSHEFQOVLSSLEN 186
QY 273 ITPTESNRRIIAILDQKQSYTPGMEKAIMETKIDSKAGNSDKYLIKEAKSDNQWAIM 332
DB 245 ELPTQD-----AVKYKGHDFM--TDVANRRNRFSEVKE-NSQAGWYGYGASSKDEYNRL 296
QY 333 VSE 335
DB 297 TKE 299

RESULT 30
US-09-059-584-12
Sequence 12, Application US/09059584
Patent No. 6440701
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,584
FILING DATE: 14-APR-1998
CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/778,570
; FILING DATE: 03-JAN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-794
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-059-584-12

Query Match
Best Local Similarity 6.6%; Score 114; DB 4; Length 682;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKPVLPVKTQNNLQACNVPOAQNASQAQNAPOAQNAPOV 60
Db |||||
QY 61 ENAPQAQNAPOVENAPQAEVTPPVPOQSQKIDGSPKIGSVKLNKEAQTLELSRFTLVD 120
Db |||||
QY 40 GNTGTSNGTGSANTPEPKY-QDVPTKEK-----DKVSSIQBPAMGYGNALSKINLHN 93
QY 121 KLGTTPKPKDVGSKKIIIEKDFVLNLSDNAEQLSG--DFLIRSDDLFGYYHDTNGK 178
Db |||||
QY 179 NLVDAADKFSQVYVYDE-KRVNDNISDKLTATYRKKEGFGVYGSNPHTKFAARISKIGD 237
Db |||||
QY 141 ----VADKNA---IGDKIKKNGKEISDEELAKQKE-----AVRKSHEFQQVLSLEN 186
QY 238 VEIKFENGQAQGSIKDEK-----DGNAEFTIKGD-----TKOLE 272
Db |||||
QY 187 KIFHSNDGTTKATTRDLKYVDYGYLLANDGN--VLTATKDLWNLGPGVGVFYNGTTAK 244
QY 273 IPTPESNRHIIAILDQNKSVTPGMEKAIMETKFDISKAGNSDQKYLIGEAQSDNQAIM 332
Db |||||
QY 245 ELPTQD-----AVKYKGHWDFM--TDVANRRNRPSEVKE-NSQAGWYYGASSKDEYNRL 296
QY 333 VSE 335
Db 297 TKE 299

RESULT 31
US-08-867-941-25
; Sequence 25, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-867-941-25

Query Match
Best Local Similarity 6.6%; Score 114; DB 2; Length 702;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKPVLPVKTQNNLQACNVPOAQNASQAQNAPOAQNAPOV 60
Db |||||
QY 21 CG--GSGGS---NPPATPTIP-----NAGSGNTGNTGAGGTDNTANA 59
QY 61 ENAPQAQNAPOVENAPQAEVTPPVPOQSQKIDGSPKIGSVKLNKEAQTLELSRFTLVD 120
Db |||||
QY 60 GNTGTSNGTGSANTPEPKY-QDVPTKEK-----DKVSSIQBPAMGYGNALSKINLHN 113
QY 121 KLGTTPKPKDVGSKKIIIEKDFVLNLSDNAEQLSG--DFLIRSDDLFGYYHDTNGK 178
Db |||||
QY 114 RODTP-----LDEKNIITLDGKKQVAGKKSPLPFLSDVENKLLDGYIAKMN-- 160
QY 179 NLVDAADKFSQVYVYDE-KRVNDNISDKLTATYRKKEGFGVYGSNPHTKFAARISKIGD 237
Db |||||
QY 161 ----VADKNA---IGDKIKKNGKEISDEELAKQKE-----AVRKSHEFQQVLSLEN 206
QY 238 VEIKFENGQAQGSIKDEK-----DGNAEFTIKGD-----TKOLE 272
Db |||||
QY 207 KIFHSNDGTTKATTRDLKYVDYGYLLANDGN--VLTATKDLWNLGPGVGVFYNGTTAK 264
QY 273 IPTPESNRHIIAILDQNKSVTPGMEKAIMETKFDISKAGNSDQKYLIGEAQSDNQAIM 332
Db |||||
QY 265 ELPTQD-----AVKYKGHWDFM--TDVANRRNRPSEVKE-NSQAGWYYGASSKDEYNRL 316
QY 333 VSE 335
Db 317 TKE 319

RESULT 32
US-08-613-009A-9
; Sequence 9, Application US/08613009A
; Patent No. 6090576
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
```

STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/613,009A
APPLICATION NUMBER: US/08/613,009A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-542
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-613-009A-9

Query Match 6.6%; Score 114; DB 3; Length 702;
Best Local Similarity 21.5%; Pred. No. 0.099;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAVPQASQVQAPQAPQAPQAPQV 60
DB 21 CG--GSGS-----NPPAPTIP-----NASGSGTGTGNAGGTDNTANA 59
QY 61 ENAPQAPQAPQVAPQAEVTPVPQSQKIDGSPDKIGSVKLNKEAQTLSESLTLD 120
DB 60 GNTGTTSGTGSANTPEPKY-QDVPTKEK-----DKVSSIQEPAMGYGMAKSKINLHN 113
QY 121 KLGTTPKFDKVGSKKIEEKDFVLNLSLDINAEQLSG--DFLIRSDDLFYGYHDTNGK 178
DB 114 RQDTP-----LDEKNIIITLQKQVAGSKSPPLFSLDVENKLLDGVIAKMN-- 160
QY 179 NLVDAADKFSQYFVWYDE-KRVNDNISDKLTATYRKKEGFGVYGSNPHTKFAARISKLD 237
DB 161 ----VADKNA-----IGDRIKKNKEISDEELAKQIKE-----AVRKSHEFQVLSLEN 206
QY 238 VEIKFENGQAGGSKDEK-----DGNAEIFTIKGD-----TKOLE 272
DB 207 KIFHSNDGTTKATRDRLKYDYGYYLANDGN--YLTATDKLNLGPGVGVFYNGTTTAK 264
QY 273 IPTESNRRIIAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLIKEAKSDNWOAIM 332
DB 265 ELPTQD-----AVKYKGHWDFM--TDVANRRNRFSEVKE-NSQAGWYGYGASSKDEYNRL 316
QY 333 VSE 335
DB 317 TKE 319

RESULT 33
US-09-074-658-25
Sequence 25, Application US/09074658
Patent No. 6184371
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-25

Query Match 6.6%; Score 114; DB 3; Length 702;
Best Local Similarity 21.5%; Pred. No. 0.099;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAVPQASQVQAPQAPQAPQAPQV 60
DB 21 CG--GSGS-----NPPAPTIP-----NASGSGTGTGNAGGTDNTANA 59
QY 61 ENAPQAPQAPQVAPQAEVTPVPQSQKIDGSPDKIGSVKLNKEAQTLSESLTLD 120
DB 60 GNTGTTSGTGSANTPEPKY-QDVPTKEK-----DKVSSIQEPAMGYGMAKSKINLHN 113
QY 121 KLGTTPKFDKVGSKKIEEKDFVLNLSLDINAEQLSG--DFLIRSDDLFYGYHDTNGK 178
DB 114 RQDTP-----LDEKNIIITLQKQVAGSKSPPLFSLDVENKLLDGVIAKMN-- 160
QY 179 NLVDAADKFSQYFVWYDE-KRVNDNISDKLTATYRKKEGFGVYGSNPHTKFAARISKLD 237
DB 161 ----VADKNA-----IGDRIKKNKEISDEELAKQIKE-----AVRKSHEFQVLSLEN 206
QY 238 VEIKFENGQAGGSKDEK-----DGNAEIFTIKGD-----TKOLE 272
DB 207 KIFHSNDGTTKATRDRLKYDYGYYLANDGN--YLTATDKLNLGPGVGVFYNGTTTAK 264
QY 273 IPTESNRRIIAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLIKEAKSDNWOAIM 332
DB 265 ELPTQD-----AVKYKGHWDFM--TDVANRRNRFSEVKE-NSQAGWYGYGASSKDEYNRL 316
QY 333 VSE 335
DB 317 TKE 319

RESULT 34
US-08-778-570B-11
Sequence 11, Application US/08778570B
Patent No. 6437096
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan

```

/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Klein, Michel H
/ TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: 6th Floor, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/778,570B
/ FILING DATE: 03-JAN-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24973
/ REFERENCE/DOCKET NUMBER: 1038-664
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 702 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-778-570B-11

```

```

Query Match 6.6%; Score 114; DB 4; Length 702;
Best Local Similarity 21.5%; Pred. No. 0.099;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKPVLPKTNLQAVPQANASQAQNAPOAQAQNAPOQ 60
DB 21 CG--GSGGS-----NPPAPTPIP-----NAGSGNTGNTAGGTDNTANA 59

QY 61 ENAPOAQAQNAQVENAQAQAEVTPPQSQKIDGDFKIGSVKLNKEAQTLESRTFLVD 120
DB 60 GNTGTNSTGTSANTPEPKY-QDVPTEKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 113

QY 121 KLGTTPPKDKVSGKKIIEKDFVLNLSIDINAQQLSG--DFLIIRSDDLFGYHYDHTNGK 178
DB 114 RQDTP-----LDEKNIITLDGKKQVAEGKKSPLPESLDVENKLLDGYIAKMN-- 160

QY 179 NLVDAADKFSQFVYVDE--KRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARISKGLD 237
DB 161 ----VADKNA-----IGDRIKKNKEISDEELAKOIKE-----AVRKSHFEQVQLSSLEN 206

QY 238 VEIKFENGQAQGSIKDEK-----DGNAEIFTIKGD-----TKOLE 272
DB 207 KIFHSNDGTTKATTRDLKVDYGYLLANDGN--YLTVKTDLKMLNLPVGVGVYNGITTTAK 264

QY 273 ITPFESNRILIIAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLIGEAQSDNQAIM 332
DB 265 ELPTQD-----AVKYGHWDPM--TDVANRRNRFSEVKE--NSQAGWYYGASSKDEYNRL 316

QY 333 VSE 335
DB 317 TKE 319

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RESULT 35
US-09-059-584-11
; Sequence 11, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:

```

```

/ APPLICANT: Myers, Lisa E
/ APPLICANT: Schryvers, Anthony B
/ APPLICANT: Harkness, Robin E
/ APPLICANT: Loomore, Sheena M.
/ APPLICANT: Du, Run-Pan
/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Klein, Michel H
/ TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: 6th Floor, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/059,584
/ FILING DATE: 14-APR-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/778,570
/ FILING DATE: 03-JAN-1997
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24973
/ REFERENCE/DOCKET NUMBER: 1038-794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 702 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-059-584-11

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Query Match 6.6%; Score 114; DB 4; Length 702;
Best Local Similarity 21.5%; Pred. No. 0.099;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKPVLPKTNLQAVPQANASQAQNAPOAQAQNAPOQ 60
DB 21 CG--GSGGS-----NPPAPTPIP-----NAGSGNTGNTAGGTDNTANA 59

QY 61 ENAPOAQAQNAQVENAQAQAEVTPPQSQKIDGDFKIGSVKLNKEAQTLESRTFLVD 120
DB 60 GNTGTNSTGTSANTPEPKY-QDVPTEKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 113

QY 121 KLGTTPPKDKVSGKKIIEKDFVLNLSIDINAQQLSG--DFLIIRSDDLFGYHYDHTNGK 178
DB 114 RQDTP-----LDEKNIITLDGKKQVAEGKKSPLPESLDVENKLLDGYIAKMN-- 160

QY 179 NLVDAADKFSQFVYVDE--KRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARISKGLD 237
DB 161 ----VADKNA-----IGDRIKKNKEISDEELAKOIKE-----AVRKSHFEQVQLSSLEN 206

QY 238 VEIKFENGQAQGSIKDEK-----DGNAEIFTIKGD-----TKOLE 272
DB 207 KIFHSNDGTTKATTRDLKVDYGYLLANDGN--YLTVKTDLKMLNLPVGVGVYNGITTTAK 264

QY 273 ITPFESNRILIIAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLIGEAQSDNQAIM 332
DB 265 ELPTQD-----AVKYGHWDPM--TDVANRRNRFSEVKE--NSQAGWYYGASSKDEYNRL 316

QY 333 VSE 335

```

Db 317 TKE 319

RESULT 36

US-09-248-796A-21477

; Sequence 21477, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 21477

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-21477

Query Match 6.5%; Score 112.5; DB 4; Length 397;

Best Local Similarity 24.7%; Pred. No. 0.059;

Matches 44; Conservative 29; Mismatches 70; Indels 35; Gaps 6;

QY 11 STFNHPKPVLPVKTQNNLQANVPQANASQANPAQANPAQANAP-----OV 60

Db 178 SEQPQPEPEPFQVELVSLVFKPQAEAGSLQPELESEPTQTEAGFKLQAESELEL 237

QY 61 ENAPQANPAQVNAQAEVTP-----PVPOQSQKIDGSPDKIGSVKLNKE-----107

Db 238 ELSEPEQ--PQEPQPPQPPDSVSQSESVSEFPQDSVSQS--ESVSELQPESEPEIRTD 294

QY 108 -----AQTLELGRFTLVDPKPPKFDKVSQKGIIEKDF---LVNLSDINAEOLS 156

Db 295 SEPEQSQSQSQSESVHKLIDTEQESNQLTRKSLDNLVINSSEEAIDSVS 352

RESULT 37

US-09-710-279-3188

; Sequence 3188, Application US/09710279

; Patent No. 6703492

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS: NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/09/710,279

; CURRENT FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3188

; LENGTH: 1279

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: amino acid sequence

US-09-710-279-3188

Query Match 6.5%; Score 112; DB 4; Length 1279;

Best Local Similarity 21.1%; Pred. No. 0.36;

Matches 81; Conservative 65; Mismatches 157; Indels 80; Gaps 18;

QY 9 SSSTPNHPKPVLPVKTQNNL--QANVPQANASQANPAQANPAQANPAQVNAAPQAO 67

Db 537 STQTKNAQKQINNDKQAEQLIQINNTPDA--TEBEKQEAATNRVNAAGLAQAIQINNNAHSTQ 595

68 NA-----PQVENAPQAEVTPPVPOPSQKI-----DG-----SFDKIG 100

596 EVNESKTSIATIKSVQNVKPKPTA--INSLTQEAANNQKTLIGNDGNATDDEKEAAKQLV 654

101 SVKLNKEAQTLL--ELSRFTLVKLGTPPKFDKVSQKII-----EKKDFLVNL-----147

655 TOKLNEIQIKIHESQDQNDVNV-----KAAQAITAKLINANAHRKQDAINTLTNLAESKK 710

148 SDINAEQ-----LSGDFLIRRSDDLFGYGYHDTNG-----KNLVDAADKFSQVFFVYD 195

711 SDIRANQDATTETKNTAIQSIDDTLAQARNNINGANTNVALVDENLEDGKQKLR--IVLS 768

196 EKRVDNISDKLTATYRKKEGVYGSNPHTKEFAARISKLGD-----VEIKFENGOAQGSI 251

769 TOTKTQAKADIAQAIGQORSTIDQONATTEBEKQEAALERLNQETNGVNDRIQAALANQV 828

252 KDEKGNAEIFTIKGDTKQLEITPTESNRII-----IAILDQNKQSYTPGMEKAIIVET 304

829 TDEKNILE--TIR-NVEPIVIVPKANEIIRKAAEQTTLINQNDATLEBKQIALGKL 885

305 KFIDSKAGNSDKYKLIIGBAKSDN 327

886 BEVKNEALNQ-----VSQAHSNN 903

RESULT 38

US-09-134-001C-5080

; Sequence 5080, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 5080

; LENGTH: 3696

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5080

Query Match 6.5%; Score 112; DB 3; Length 3696;

Best Local Similarity 21.1%; Pred. No. 1.7;

Matches 81; Conservative 65; Mismatches 157; Indels 80; Gaps 18;

QY 9 SSSTPNHPKPVLPVKTQNNL--QANVPQANASQANPAQANPAQANPAQVNAAPQAO 67

Db 1935 STQTKNAQKQINNDKQAEQLIQINNTPDA--TEBEKQEAATNRVNAAGLAQAIQINNNAHSTQ 1993

68 NA-----PQVENAPQAEVTPPVPOPSQKI-----DG-----SFDKIG 100

1994 EVNESKTSIATIKSVQNVKPKPTA--INSLTQEAANNQKTLIGNDGNATDDEKEAAKQLV 2052

101 SVKLNKEAQTLL--ELSRFTLVKLGTPPKFDKVSQKII-----EKKDFLVNL-----147

2053 TOKLNEIQIKIHESQDQNDVNV-----KAAQAITAKLINANAHRKQDAINTLTNLAESKK 2108

148 SDINAEQ-----LSGDFLIRRSDDLFGYGYHDTNG-----KNLVDAADKFSQVFFVYD 195

2109 SDIRANQDATTETKNTAIQSIDDTLAQARNNINGANTNVALVDENLEDGKQKLR--IVLS 2166

196 EKRVDNISDKLTATYRKKEGVYGSNPHTKEFAARISKLGD-----VEIKFENGOAQGSI 251

2167 TOTKTQAKADIAQAIGQORSTIDQONATTEBEKQEAALERLNQETNGVNDRIQAALANQV 2226

252 KDEKGNAEIFTIKGDTKQLEITPTESNRII-----IAILDQNKQSYTPGMEKAIIVET 304

Query Match 6.4%; Score 111.5; DB 2; Length 403;
Best Local Similarity 21.8%; Pred. No. 0.074;
Matches 90; Conservative 53; Mismatches 146; Indels 123; Gaps 18;

QY 4 SGGSGSSSTNHPKPLV-----PKTNNLQANVPQANASQ----- 41
Db 10 SGPVKATAPVGGPRVLVTQPFQCPNLPVNSGQARVLCPSNSSORVPLQAKLVSSHK 59
QY 42 -AQNAPQANAPQANAPQVENAP--QAQNAPO-----VENAPQAEVTPPVPOQSQKID 93
Db 70 PVQN--QKQQLQATSVPHVPSRPLNNTQSKQPLPSAPENNPEELASKQKNEESKKRQ 127
QY 94 GSPD-----KIGSVKLNKEAQTLELSRFTLVDLKLTGTPKPKDKVSGKXIIEEKDF 142
Db 128 WALEDFEIGRPLGKRGFNGVYLAREQO-----SKFIALKLVLFKAQLEKAGVEHQLEREVE 183
QY 143 LVNLNSDINAEQLSGDFLIIRSDOLFYGYYHDTNGKNLVDAADKFSQYFVYDEKEVNDN 202
Db 184 IQSHLRHPNLR-----YGFHDATRVYLI---LEYAPLGTIVYRELQKLSK 227
QY 203 ISDKLTATY-----RKKEGFVYGSNPHYK--EF-----AARI 232
Db 228 FDEQRTATYITELANALSYCHSKRVIHRDIKPENLILGSAGELKIADFGNSVHAPSSRRT 287
QY 233 SKLGDVEIKFENGQAQGSIXDEK-----DGNAEIFTIKGDTKOLE 272
Db 288 TLGTLDY-LPPENIEGRMEDEKVDLWSLGLVCEYELVKGKPPPEANTYQETK-RISRYE 345
QY 273 IT-----PTESNRITIIILDONOKSYTPGMEKAIMETKFI---DSKAGNSDQK 317
Db 346 FTFPDFVTEGARDLISRLKXHPFSQRP-MLREVLEHFWITANSKSPSCNQNK 396

Search completed: December 17, 2004, 16:02:42
Job time : 51.7763 secs

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OM protein - protein search, using sw model

Run on: December 17, 2004, 15:52:28 ; Search time 203.087 Seconds
(without alignments)
595.271 Million cell updates/sec

Title: US-10-696-544-2
Perfect score: 1734
Sequence: 1 CGSGSGSSSPNHPKPVLPVL.....YLIGSAKSDNQAINVSEKK 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1734	100.0	337	8	Adp82911 rPlpE. 8/
2	221.5	12.8	335	7	Adf29249 Bacterial
3	221.5	12.8	335	7	Adg32458 Pasteurel
4	219	12.6	43	8	Adp82921 Mannheimi
5	186.5	10.8	1164	3	Aay84463 Amino aci
6	178.5	10.3	1135	3	Aay84460 Amino aci
7	177	10.2	984	3	Aay84481 Amino aci
8	177	10.2	1164	2	Aaw40537 Group B s
9	177	10.2	1164	3	Aay84459 Amino aci
10	173	10.0	984	2	Aar85782 Group B S
11	173	10.0	1093	2	Aaw40540 Mutant C-
12	173	10.0	1099	2	Aaw40538 Mutant C-
13	173	10.0	1128	2	Aaw40539 Mutant C-
14	173	10.0	1128	3	Aay84461 Amino aci
15	173	10.0	1164	2	Aar85781 Group B S
16	173	10.0	1164	2	Aaw40541 Mutant C-
17	168	9.7	1129	3	Aay84462 Amino aci
18	165	9.5	348	2	Aar54665 Outer mem
19	147	8.5	837	4	Abbs58463 Drosophil
20	140.5	8.1	730	2	Aay43385 S. pneumo
21	138.5	8.0	367	2	Aar54666 Outer mem
22	135.5	7.8	1192	4	Abbs58462 Drosophil
23	131	7.6	356	8	Adq30503 Codon-opc
24	131	7.6	478	3	Aab07288 Human IL-
25	129.5	7.5	4365	6	Abu02252 S. pneumo

26	127	7.3	448	8	ADM16778
27	127	7.3	485	2	AAW5462
28	127	7.3	485	2	AAW5462
29	127	7.3	485	2	AAW5462
30	126	7.3	254	4	ABG16808
31	125.5	7.2	1036	6	ABU36235
32	124	7.2	631	2	AAW08970
33	124	7.2	631	2	AAW51784
34	124	7.2	631	2	AAW54128
35	124	7.2	631	2	AAW80366
36	124	7.2	917	3	AAW53920
37	124	7.2	921	7	AAW58793
38	124	7.2	930	4	ABG16236
39	123.5	7.1	861	4	ABW59487
40	122	7.0	599	6	ABU35643
41	122	7.0	631	2	AAW77896
42	121.5	7.0	3111	4	ABW60327
43	121	7.0	912	8	ADJ76291
44	121	7.0	1308	7	ADH88703
45	120.5	6.9	287	7	ADF28364

ALIGNMENTS

RESULT 1
ADP82911
ID ADP82911 standard; protein; 337 AA.
XX
AC ADP82911;
XX
DT 12-AUG-2004 (first entry)
XX
DE rPlpE.
XX
KW recombinant PlpE; Antibacterial; Immunostimulant;
XX bovine respiratory disease; vaccine.
XX Mannheimia haemolytica.
OS
PN WO2004041182-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034574.
XX
PR 30-OCT-2002; 2002US-0422305P.
XX (OKLA) UNIV OKLAHOMA STATE.
PA Confer AW, Ayalew S, Murphy GL, Pandher K;
XX WPI; 2004-411400/38.
DR N-PSDB; ADP82910.
XX
PT New vaccine compositions comprising a recombinant PlpE outer membrane protein of M. haemolytica optionally in combination with at least one other antigen against M. haemolytica, useful for preventing bovine respiratory disease.
PS Example 1; SEQ ID NO 2; 48pp; English.
XX
CC The present invention relates to a vaccine composition against infection of M. haemolytica in cattle comprises: recombinant PlpE outer membrane protein of M. haemolytica or its antigenic subunit; or a recombinant PlpE outer membrane protein of M. haemolytica or its antigenic subunits, in combination with at least one other antigen against M. haemolytica; and a pharmaceutical carrier or diluent. The vaccine is useful against infection of M. haemolytica in cattle, or for inducing an immune response in cattle to provide immune protection against bovine respiratory disease and/or shipping fever to an at-risk bovine. The new vaccine provides better protection or immunization than existing commercially available vaccines. The present sequence represents rPlpE.

```

XX SQ Sequence 337 AA;
    Query Match      100.0%; Score 1734; DB 8; Length 337;
    Best Local Similarity 100.0%; Pred. No. 1.3e-140;
    Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGSGSGSGSSSTPNHPKPVLPVKTQNNLQACNVPOQAQNAQNAQNAQNAQNAQV 60
DB 1 CGSGSGSGSSSTPNHPKPVLPVKTQNNLQACNVPOQAQNAQNAQNAQNAQV 60

QY 61 ENAPQAQNAPOVENAPOAEVTPVPQSQKIDGSGFDKIGSVKLNKEAQTLELSRFLVND 120
DB 61 ENAPQAQNAPOVENAPOAEVTPVPQSQKIDGSGFDKIGSVKLNKEAQTLELSRFLVND 120

QY 121 KLGTPPKFDKVSQKIIIEKDFVLNLSDNAEQLSGDGLIRRSDDLFGYGYHDTNGKNL 180
DB 121 KLGTPPKFDKVSQKIIIEKDFVLNLSDNAEQLSGDGLIRRSDDLFGYGYHDTNGKNL 180

QY 181 VDAADKFSQYVVDYDEKRVNDNISDKLTATYRKKEGFGVGSNPHTKFAARIISKLGDVEI 240
DB 181 VDAADKFSQYVVDYDEKRVNDNISDKLTATYRKKEGFGVGSNPHTKFAARIISKLGDVEI 240

QY 241 KFENGQAQSGSIKDEKGNABEFTTKGDTKQLEITPTESNRIIILDQNKSYTPGWKEA 300
DB 241 KFENGQAQSGSIKDEKGNABEFTTKGDTKQLEITPTESNRIIILDQNKSYTPGWKEA 300

QY 301 IMETKFDISKAGNSDQKYLIGEAKSDNWQAIMVSEKK 337
DB 301 IMETKFDISKAGNSDQKYLIGEAKSDNWQAIMVSEKK 337

RESULT 2
ADF22249
ID ADF229249 standard; protein; 335 AA.
XX AC ADF229249;
XX DT 12-FEB-2004 (first entry)
XX DE Bacterial virulence associated Pasteurella multocida protein PM1517.
XX KW antibacterial; vaccine; mutant; Gram negative bacterium; mutation;
XX KW attenuated virulence; immunogenic composition; passive immunization;
XX KW insertion site; transposon tagged mutagenesis.
XX OS Pasteurella multocida.
XX FN EPI350796-A1.
XX PD 08-OCT-2003.
XX PF 05-APR-2002; 2002EP-00290861.
XX PR 05-APR-2002; 2002EP-00290861.
XX PA (MERI-) MERIAL.
XX PI Crooke HR, Shea JE, Feldman RG, Goutebroze SG, Le Gros F;
XX WPI; 2003-781146/74.
XX DR N-PSDB; ADF22248.
XX CC New attenuated mutant of a Gram-negative bacteria, useful for the
XX CC production of immunogenic or vaccine compositions for the prevention of
XX CC bacterial infections, particularly Gram negative bacteria.
XX PS Example 4; SEQ ID NO 41; 96pp; English.
XX CC The invention relates to a mutant Gram negative bacterium (Pasteurella
XX CC multocida) comprising a mutation in a nucleotide sequence which codes for
XX CC a polypeptide having an identity which is equal or more than 70%, 75%,
XX CC 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% with an amino acid sequence

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CC encoded by any of 29 fully defined sequences of 267-2832 bp, given in the
CC specification, the mutation resulting in attenuated virulence of the
CC bacterium. The attenuated mutant is useful for the production of
CC immunogenic or vaccine compositions for the prevention of bacterial
CC infections, particularly Gram negative bacteria. The antibody preparation
CC is useful for the production of a passive immunization composition of a
CC therapeutic composition against Gram-negative bacteria. This sequence
CC represents the Pasteurella multocida protein PM0773 which is involved in
CC bacterial virulence.
XX Sequence 335 AA;
SQ Query Match      12.8%; Score 221.5; DB 7; Length 335;
    Best Local Similarity 22.8%; Pred. No. 2e-10;
    Matches 79; Conservative 58; Mismatches 160; Indels 49; Gaps 10;

QY 2 CGSGSGSGSSSTPNHPKPVLPVKTQNNLQACNVPOQAQNAQNAQNAQNAQV 61
DB 23 CGSGSAGNADRVBEK-----AQPV---QSNSEPSAPIKNPTNTATNDSLHD 67

QY 52 NAPQAQNAPOVENAPOAEVTPVPQSQKIDGSGF-----DKIGSVKLNKEAQTLELS 114
DB 68 KLSMSHSDTSKENSQSSFKAPLEQEKQPAQENLTWTGHHVSEVGNASNNVDKDNVTV- 126

QY 115 RFTLV---DKLGTPPKFDKVSQKIIIEKDFVLNLSDNAEQLSGDGLIRRSDDLFGY 171
DB 127 -FTFVKYNSQYNDPVPFDKTKTQS-----KTSISLVDGKNENKEDYVNFCLKDALF--- 175

QY 172 YHDTNGKNLVDAAADKFSQYFVYDEKRVNDNISDKLTATYRKKEGFGVGSNPHTKFAAR 231
DB 176 YGSGYQPSADYKVKYKNIYIAIKPDAINNENLALTATYQEDGFTYSLSDVNRVYGE 235

QY 232 -ISKLGVDVEIKFENGQAQSGSIKDEKGNABEFTTKGDTKQLEITPTESNRIIILDQNK 290
DB 236 YIPQVGNVTLTFRNGKIYGEIYRYNRGRDDLFOISGEGQNTLITPHK-----DNPH 286

QY 291 KSYTPGMEKAIKMETKFDISKAGNSDQKYLIGEAKSDNWQAIMVSEK 336
DB 287 KLSPTGPDNMAELNFIN--AEKTDKKYVGVGVGAKEYYGLLFAEK 330

RESULT 3
ADG32458
ID ADG32458 standard; protein; 335 AA.
XX AC ADG32458;
XX DT 26-FEB-2004 (first entry)
XX DE Pasteurella multocida PM1517 protein, a homologue of PM70 SeqID 41.
XX KW immunogenic; vaccine; bacterial infection; Pasteurellaceae; immunogen;
XX KW allergen; growth factor; cytokine; antibacterial;
XX KW transposon insertion site; attenuated gram negative bacteria.
XX OS Pasteurella multocida.
XX PN WO2003086277-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010308.
XX PR 05-APR-2002; 2002US-0370282P.
XX PR 03-APR-2003; 2003US-00406686.
XX PA (MERI-) MERIAL LLC.
XX PI Crooke HR, Shea JE, Feldman RG, Goutebroze SG, Legros F;
XX WPI; 2003-845250/78.
XX DR N-PSDB; ADG32457.
XX CC

```

PT New mutant gram negative bacterium having attenuated virulence, useful
PT for preparing a composition or vaccine for preventing bacterial
PT infections.
XX
XX
XX Example 4; SEQ ID NO 41; 170pp; English.
XX
XX This invention relates to novel live attenuated gram negative bacteria
CC useful for immunogenic compositions and in vaccines to prevent bacterial
CC infections. Specifically, it refers to a mutant gram negative bacterium
CC from the Pasteurellaceae family, having a mutation in a first nucleotide
CC sequence that codes for a first polypeptide, and results in the bacterium
CC having attenuated virulence. This mutation can be a deletion, insertion
CC or replacement of nucleic acids in a regulatory element or coding
CC sequence of a gene that encodes an immunogen such as a viral, parasitic
CC or bacterial agent, allergen, growth factor, therapeutic protein or
CC cytokine. The present invention describes a method for attenuating live
CC bacteria that reduces or abolishes pathogenicity, decreases bacterial
CC growth rate and thereby prevents cell death. Accordingly, these
CC compositions have antibacterial activity and can be administered in an
CC antibody preparation. This polypeptide sequence is a homologue of the
CC Pasteurella multocida PM70 protein that is disrupted by insertion of a
CC transposon to generate a mutant of the invention.
XX
XX
XX Sequence 335 AA;
Query Match 12.8%; Score 221.5; DB 7; Length 335;
Best Local Similarity 22.8%; Pred. NO. 2e-10;
Matches 79; Conservative 58; Mismatches 160; Indels 49; Gaps 10;
QY 2 GSGSGSSSTPHKPVLPVKTQNNLQAVPQANASQANAPQANAPQANAPQVE 61
DB 23 GGGSGAGNADRVVEK-----AQPV---QSNSEPSAPTINKTNTATNDSLHD 67
QY 62 NAPQANAPQVENAPQAEVTPVPQSQKIDGSF-----DKIGSVKLKKEAQTLELS 114
DB 68 KLSMSHSDTSKENSQSSFKAPLEQKQPAQENLTWYGVHSEGVNANNVYDKDNVTV- 126
QY 115 RPTLV---DKLGTTPFKDQVSGKKIIEKDFLVNLSDINAEQLSDFLIRSDDLFYGY 171
DB 127 -FTFVKYNSQYNDPVDFTKTQS-----KTISLVGKGNENKEDYNYFTLKDALF--- 175
QY 172 YHDTNGKLVDAADKFSQVYVDEKRVNDNISDKLTATYRKKEGFPVYGSNPHTEFAAR 231
DB 176 YGSGYQSPSDYKKVKNVYIATKPAINNENLNALTATYQEDGFIYSLSDVNRVGE 235
QY 232 -ISKLGVEIKFENGQAQSGIKDEKGNAEIETIKGTQKLEITPTPESNRIIAILDQKQ 290
DB 236 YIPQYGNVLTFRNGKIYGIYRNGRDLFQLSGEGQNLITPHK-----DNPH 286
QY 291 KSYTPGWEKAIMETKFTDSKAGNSDKYLLIGEAQSDNQWQAIMVSEK 336
DB 287 KLSPTGPDNMAMELNFIN--AEKTDKYYVGVGKAEKYYGLLFAEK 330
RESULT 4
ADP82921
ID ADP82921 standard; peptide; 43 AA.
XX
XX AC ADP82921;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Mannheimia haemolytica epitope #2.
XX
XX DE recombinant PlpE; Antibacterial; Immunostimulant;
XX KW bovine respiratory disease; vaccine; ds.
XX
XX OS Mannheimia haemolytica.
XX
XX OS Mannheimia haemolytica.
XX
XX PN WO2004041182-A2.
XX
XX PD 21-MAY-2004.
XX

PF 30-OCT-2003; 2003WO-US034574.
XX
XX PR 30-OCT-2002; 2002US-0422305P.
XX
XX PA (OKLA) UNIV OKLAHOMA STATE.
XX
XX PI Confer AW, Ayalew S, Murphy GL, Pandher K;
XX
XX DR WPI; 2004-411400/38.
XX
XX PT New vaccine compositions comprising a recombinant PlpE outer membrane
PT protein of M. haemolytica optionally in combination with at least one
PT other antigen against M. haemolytica, useful for preventing bovine
PT respiratory disease.
XX
XX PS Example 2; SEQ ID NO 12; 48pp; English.
XX
XX CC The present invention relates to a vaccine composition against infection
CC of M. haemolytica in cattle comprises: recombinant PlpE outer membrane
CC protein of M. haemolytica or its antigenic subunit; or a recombinant PlpE
CC outer membrane protein of M. haemolytica or its antigenic subunits, in a
CC combination with at least one other antigen against M. haemolytica; and a
CC pharmaceutical carrier or diluent. The vaccine is useful against
CC infection of M. haemolytica in cattle, or for inducing an immune response
CC in cattle to provide immune protection against bovine respiratory disease
CC and/or shipping fever to an at-risk bovine. The new vaccine provides
CC better protection or immunization than existing commercially available
CC vaccines. The present sequence represents Mannheimia haemolytica PlpE
CC epitope region, out of a total of 8 regions found.
XX
XX
XX Sequence 43 AA;
Query Match 12.6%; Score 219; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. NO. 1.9e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 QNASQANAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQAE 79
DB 1 QNASQANAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQAE 43
RESULT 5
AY84463
ID AY84463 standard; protein; 1164 AA.
XX
XX AC AY84463;
XX
XX DT 25-JUL-2000 (first entry)
XX
XX DE Amino acid sequence of a C-beta protein.
XX
XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;
XX immune response.
XX
XX OS Streptococcus agalactiae.
XX
XX PN WO200015760-A1.
XX
XX PD 23-MAR-2000.
XX
XX PF 17-SEP-1999; 99WO-US021643.
XX
XX PR 17-SEP-1998; 98US-0100859P.
XX PR 19-JUL-1999; 99US-0144324P.
XX PR 15-SEP-1999; 99US-0154017P.
XX
XX PA (NVA-) NORTH AMERICAN VACCINE INC.
XX
XX PI Long-Rowe KO, Blake MS;
XX
XX DR WPI; 2000-271404/23.
XX
XX DR N-PSDB; AAA12456.
XX

AA84481;
25-JUL-2000 (first entry)
Amino acid sequence of a fragment of the C-beta protein.
C-beta protein; bactericidal; gram positive bacteria; vaccine;
immune response.
Streptococcus agalactiae.
WO200015760-A1.
23-MAR-2000.
17-SEP-1999; 99WO-US021643.
17-SEP-1998; 98US-0100859P.
19-JUL-1999; 99US-0144324P.
15-SEP-1999; 99US-0154017P.
(NAVA-) NORTH AMERICAN VACCINE INC.
Long-Rowe KO, Blake MS;
WPI; 2000-271404/23.
Obtaining substantially pure C-beta protein or fragment and/or mutant for
eliciting antibodies which are bactericidal to gram positive bacteria,
useful in vaccines.
Disclosure; Page 153-156; 171pp; English.
The specification describes a process for obtaining a substantially pure
C-beta protein. The process comprises obtaining the C-beta protein in
cell extracts, subjecting the C-beta protein to ion-exchange
chromatography and collecting the C-beta protein-containing fractions,
pooling and diluting the fractions, and subjecting the fractions to
ligand affinity chromatography and collection. The C-beta protein
fragments are useful for eliciting antibodies which are bactericidal to
gram positive bacteria with complement alone and therefore is useful in a
(combination) vaccine together with a pharmaceutically acceptable carrier
(and/or optionally at least two protein fragments or peptide-
polysaccharide conjugates). The vaccine therefore is useful in a method
for inducing an immune response in a mammal. The present sequence
represents a Streptococcus agalactiae C-beta protein fragment
Sequence 984 AA;
Query Match 10.2%; Score 177; DB 3; Length 984;
Best Local Similarity 23.6%; Pred. No. 6e-06;
Matches 81; Conservative 44; Mismatches 114; Indels 104; Gaps 15;
12 TPNHPKPVLPKTONNLOQNVPOAQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
649 TPTDKPIELPQAPDTQAPDTHPVPSKAPAPVPESPKTPEAPHPVPSKAPAPR 708
72 VENAPQAEVTPPVQ---PQSQIDGSDFKIGSVKLNKEAQTLLESLRFTLVKLGTPPK 127
709 VPESPKTPEAPHPVPSKTPAPKIP-----KPKTPDVPKLPDVPKLPDVPK 756
128 -----FDKVGK---KIEEK--DFVLNLSNDINAEQLSGDFLIRS 164
757 LPDAPKLPDGLNKVGQAVFTSDGNTKVTVDKFTDADKLHLKEVTTKELADKIA---- 812
165 DDLFVGYHDNGKLVDAADKFSQYFVVD-----EKRYNDNISDKLTATYRKKEG 216
813 -----HKTGGTV-----RVFLSLUSKGGKTHVNGERTVRLALGQTGSDV 853
217 FVYGSNPHTEFAARISKLGVE---IKFNGQAQGSIKDEKGNABIFITKGDTKOLEI 273
854 HVY-----HVKE-----NGDLERIPSKVENGQV-----FKTNHFLFALKULSKQNV 897

QY 274 TPTESNRILIIILDQNOKSYTPGMEKALMET---KPIDSKAGN 313
DB 898 TTPKQT-----KPSTQGSQVEIABSQTGKF-QSKAAN 928
RESULT 8
AAW40537
ID AAW40537 standard; protein; 1164 AA.
XX AAW40537;
XX 17-OCT-2003 (revised)
DT 28-AUG-1998 (first entry)
XX Group B streptococcal C-beta protein.
XX C-beta protein; beta antigen; vaccine; group B Streptococcus.
OS Streptococcus sp; strain A909.
XX Key Location/Qualifiers
FH Peptide 1..37
FT Protein 38..1164
FT Protein 38..1164
FT Region 200..213
FT Domain 1132..1164
FT /label= Iga_binding_region
FT /label= Transmembrane_domain
XX WO9809648-A1.
XX 12-MAR-1998.
XX 05-SEP-1997; 97WO-US015319.
XX 06-SEP-1996; 96US-0024707P.
XX (NAVA-) NORTH AMERICAN VACCINE INC.
XX Tai JY, Blake MS;
XX WPI; 1998-193324/17.
XX N-PSDB; AAW11344.
XX Group B streptococcal C-beta proteins - having amino acid substitutions to
reduce immunoglobulin A binding while retaining antigenicity, for use in
vaccines.
XX Claim 1; Fig 1; 59pp; English.
XX This polypeptide comprises the wild-type C-beta protein, or beta antigen,
of a group B Streptococcus that binds to human IGA. The invention relates
to mutant C-beta proteins (see AAW40538-41) of formula A(X1-X12)B, where
A comprises amino acids 1-164 of mature C-beta protein, B comprises amino
acids 177 to 1096-1127 of mature C-beta, and X1-X12 are each selected
independently from Ala, Val, Leu, Ile, Pro, Met, Phe, Trp, a bond, or the
corresponding amino acid residue from B-beta protein, provided that at
least one of X1 to X12 is other than the wild-type amino acid and that
the LPXG motif may be missing. Claimed mutant C-beta proteins also have
hydrophobic amino acid residues 1108-1116 replaced by non-hydrophobic
amino acid residues, and at least one of amino acid residues 521-541
(preferably 533-541) either deleted or altered. Vectors comprising
polynucleotides encoding such proteins, and transformed host cells, are
claimed. The mutant C-beta proteins have reduced IGA binding while
retaining most of the antigenicity of the wild-type protein. They can be
used alone, or conjugated to a polysaccharide, in vaccines for use
against group B Streptococci (claimed). (Updated on 17-OCT-2003 to
standardise OS field)
XX Sequence 1164 AA;
XX Query Match 10.2%; Score 177; DB 2; Length 1164;

CC known to bind to the Fc region of IGA immunoglobulins in a non-immune
 CC manner. The portion of the beta antigen gene which encodes the IGA
 CC binding function has been identified and removed to give a truncated beta
 CC antigen gene whose product (AAW4542) has no IGA binding activity but
 CC does immunoreact with monospecific anti-beta antigen antisera raised
 CC against wild-type beta antigen protein. The non-IGA binding form of the
 CC beta antigen can be used as a component in a human vaccine to protect
 CC against group B Streptococcal infection
 CC
 XX Sequence 984 AA;

Query Match 10.0%; Score 173; DB 2; Length 984;
 Best Local Similarity 23.3%; Pred. No. 1.3e-05;
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHPKVLVPTKQNNLQANVPOAQNASQAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
 DB 649 TDTPKIPLPQADPTQADPTHPVPSKAPAPRVPSKTPPEAPHVPSKAPAPR 708
 QY 72 VENAPQAEVTPPVQ-----PQSQKIDGSPDKIGSVKLNKEAQTLELSRFTLVLDLGTTPK 127
 DB 709 VPESKTPPEAPHVPSKTPPEAPKIP-----EPPKTPDVPKLPDVPKLPDVPK 756
 QY 128 -----FDKVSCK---KIIEEK--DFLVNLSDINAEQSGDFLIRRS 164
 DB 757 LPDAPKLPDGLNKGQAVFTSTDGNTKVTWVFDKPTDADKLHLKEVTTKELADKIA---- 812
 QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVYD-----EKRVDNISDKLTATYRKKEG 216
 DB 813 -----HKTGGTV-----RVFDLSLKGKETHVNGERTVRLALGQTGSDV 853
 QY 217 FVYGSNPHTEFAARISKLGDE--IKFENGQAQGSIKDEKGNABEFTIKGDTKQLEI 273
 DB 854 HVY-----HVKE-----NGDLERIPSKVENGQV-----FKTNHFSLFAIKTILSKQNV 897
 QY 274 TPTESNRIIILDQNKSVTPGMEKAIMET---KFIDSKAGN 313
 DB 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928

RESULT 11
 AAW40540
 ID AAW40540 standard; protein; 1093 AA.

XX AC AAW40540;
 XX 28-AUG-1998 (first entry)
 XX Mutant C-beta protein dgb1.
 XX C-beta protein; beta antigen; vaccine; group B Streptococcus.
 XX Streptococcus sp; strain A909.
 XX Synthetic.
 XX WO9809648-A1.
 XX 12-MAR-1998.
 XX 05-SEP-1997; 97WO-US015319.
 XX 06-SEP-1996; 96US-0024707P.
 XX (NAVA-) NORTH AMERICAN VACCINE INC.
 XX Tai JY, Blake MS;
 XX WPI; 1998-193324/17.
 XX N-PSDB; AAV11347.

XX Group B streptococcal Cbeta proteins - having amino acid substitutions to
 PT reduce immunoglobulin A binding while retaining antigenicity, for use in
 PT vaccines.

XX Disclosure; Fig 8A-C; 59pp; English.
 XX Group B Streptococcus C-beta mutant protein dgb1 has 0% of the IGA
 CC binding activity of the native C-beta protein (see AAW40537). It is
 CC encoded by mutated C-beta protein DNA (see AAV11347) in which codons 168-
 CC 175 are deleted and replaced by a codon for Glu and a codon for Ala.
 CC These residues are in the IGA binding domain of the C-beta protein. The
 CC IGA binding ability of C-beta appears to require dimerisation of the
 CC protein. The invention relates to mutant C-beta proteins that have a
 CC reduced or eliminated ability to bind human IGA but which retain the
 CC antigenicity of the wild-type protein. Such proteins can be used in
 CC vaccines for use against group B streptococci. Claimed mutant proteins
 CC have mutations in the IGA binding region of C-beta
 XX
 XX Sequence 1093 AA;

Query Match 10.0%; Score 173; DB 2; Length 1093;
 Best Local Similarity 23.3%; Pred. No. 1.5e-05;
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHPKVLVPTKQNNLQANVPOAQNASQAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
 DB 787 TDTPKIPLPQADPTQADPTHPVPSKAPAPRVPSKTPPEAPHVPSKAPAPR 846
 QY 72 VENAPQAEVTPPVQ-----PQSQKIDGSPDKIGSVKLNKEAQTLELSRFTLVLDLGTTPK 127
 DB 847 VPESKTPPEAPHVPSKTPPEAPKIP-----EPPKTPDVPKLPDVPKLPDVPK 894
 QY 128 -----FDKVSCK---KIIEEK--DFLVNLSDINAEQSGDFLIRRS 164
 DB 895 LPDAPKLPDGLNKGQAVFTSTDGNTKVTWVFDKPTDADKLHLKEVTTKELADKIA---- 950
 QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVYD-----EKRVDNISDKLTATYRKKEG 216
 DB 951 -----HKTGGTV-----RVFDLSLKGKETHVNGERTVRLALGQTGSDV 991
 QY 217 FVYGSNPHTEFAARISKLGDE--IKFENGQAQGSIKDEKGNABEFTIKGDTKQLEI 273
 DB 992 HVY-----HVKE-----NGDLERIPSKVENGQV-----FKTNHFSLFAIKTILSKQNV 1035
 QY 274 TPTESNRIIILDQNKSVTPGMEKAIMET---KFIDSKAGN 313
 DB 1036 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 1066

RESULT 12
 AAW40538
 ID AAW40538 standard; protein; 1099 AA.
 XX AC AAW40538;
 XX 28-AUG-1998 (first entry)
 XX Mutant C-beta protein dgb2.
 XX C-beta protein; beta antigen; vaccine; group B Streptococcus.
 XX Streptococcus sp; strain A909.
 XX Synthetic.
 XX WO9809648-A1.
 XX 12-MAR-1998.
 XX 05-SEP-1997; 97WO-US015319.
 XX 06-SEP-1996; 96US-0024707P.
 XX (NAVA-) NORTH AMERICAN VACCINE INC.
 XX Tai JY, Blake MS;

DR WFI; 1998-193324/17.
 DR N-PSDB; AAV11345.
 XX
 XX Group B streptococcal C-beta proteins - having amino acid substitutions to
 PT reduce immunoglobulin A binding while retaining antigenicity, for use in
 PT vaccines.
 XX
 XX Disclosure; Fig 6A-C; 59pp; English.
 XX
 XX Group B Streptococcus C-beta mutant protein dqb2 has only 60% of the IGA
 CC binding activity of the native C-beta protein (see AAW40537). It is
 CC encoded by mutated C-beta protein DNA (see AAV11345) in which the Lys-170
 CC and Lys-175 codons of the mature C-beta protein coding region are
 CC replaced by Ala codons. These residues are in the IGA binding domain of
 CC the C-beta protein. The invention relates to mutant C-beta proteins that
 CC have a reduced or eliminated ability to bind human IGA but which retain
 CC the antigenicity of the wild-type protein. Such proteins can be used in
 CC vaccines for use against group B streptococci. Claimed mutant proteins
 CC have mutations in the IGA binding region of C-beta
 XX
 XX Sequence 1099 AA;
 Query Match 10.0%; Score 173; DB 2; Length 1099;
 Best Local Similarity 23.3%; Pred. No. 1.5e-05;
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;
 QY 12 TPNHPKPLVPTQNNLOAQNVPQQAQNASQNAQNAPOAQNAPQOVENAPQANAPQ 71
 DB 793 TPTDTPKIPQLPQADPTQAPDTPHVPSPKAPAPRVPEPKTPPEAHPVPSKAPAPR 852
 QY 72 VENAPOAEVTPVPO-----PQSQKIDGSFDKIGSVKLNKEAQTLELSRFTLVDKLGP 127
 DB 853 VPESKTPPEAHPVPSKTPPEAPKIP-----EPKTPDVPKLPDVPKLPDVPK 900
 QY 128 -----FDKVSQK---KIIEEK---DFLVNLSDINAEQSGDFLIRRS 164
 DB 901 LPDAPKLPDGLNKVQAVFTSTGNTKVTVVFDKPTDADKLHLKEVTTKELADKIA--- 956
 QY 165 DDLFYGYVHDNGKLVDAADKFSQYFVVD-----EKRVDNLSDKLTATYRKKEG 216
 DB 957 -----HKTGGGTV-----RVFSLSKGKGKETHVNGERTVRLALQGTGSDV 997
 QY 217 FVYGSNPHTKFAARISKLGDE---IKFENGQAQGSIKDEKGNABIFTIKGDTKQLEI 273
 DB 998 HVY---HVKE-----NGDLERIPSKVGVQV-----FKTNHFSLSFAIKLTSLKQNV 1041
 QY 274 TPTESNRILIIALDONQKSYTPGMEKAIMET---KFDTSKAGN 313
 DB 1042 TPKQOT-----KPSTQGSQVEIASQTGKF-QSKAAN 1072
 RESULT 13
 AAW40539
 ID AAW40539 standard; protein; 1128 AA.
 XX
 XX AAW40539;
 AC
 XX 28-AUG-1998 (first entry)
 DT
 XX Mutant C-beta protein nv34qp.
 XX
 XX C-beta protein; beta antigen; vaccine; group B Streptococcus.
 KW
 XX Streptococcus sp; strain A909.
 OS
 OS Synthetic.
 XX
 XX WO9809648-A1.
 XX
 XX 12-MAR-1998.
 PD
 XX 05-SEP-1997; 97WO-US015319.
 PF
 XX 06-SEP-1996; 96US-0024707P.
 PR

(NAVA-) NORTH AMERICAN VACCINE INC.
 Tai JY, Blake MS;
 WFI; 1998-193324/17.
 N-PSDB; AAV11346.
 Group B streptococcal C-beta proteins - having amino acid substitutions to
 reduce immunoglobulin A binding while retaining antigenicity, for use in
 vaccines.
 Disclosure; Fig 7A-C; 59pp; English.
 Group B Streptococcus C-beta mutant protein nv34qp has only 10% of the
 IGA binding activity of the native C-beta protein (see AAW40537). It is
 encoded by mutated C-beta protein DNA (see AAV11346) in which the Gln-167
 and Gln-174 codons of the mature C-beta protein coding region are
 replaced by Pro codons. These residues are in the IGA binding domain of
 the C-beta protein. The IGA binding ability of C-beta appears to require
 dimerisation of the protein. The invention relates to mutant C-beta
 proteins that have a reduced or eliminated ability to bind human IGA but
 which retain the antigenicity of the wild-type protein. Such proteins can
 be used in vaccines for use against group B streptococci. Claimed mutant
 proteins have mutations in the IGA binding region of C-beta
 Sequence 1128 AA;
 Query Match 10.0%; Score 173; DB 2; Length 1128;
 Best Local Similarity 23.3%; Pred. No. 1.6e-05;
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;
 QY 12 TPNHPKPLVPTQNNLOAQNVPQQAQNASQNAQNAPOAQNAPQOVENAPQANAPQ 71
 DB 793 TPTDTPKIPQLPQADPTQAPDTPHVPSPKAPAPRVPEPKTPPEAHPVPSKAPAPR 852
 QY 72 VENAPOAEVTPVPO-----PQSQKIDGSFDKIGSVKLNKEAQTLELSRFTLVDKLGP 127
 DB 853 VPESKTPPEAHPVPSKTPPEAPKIP-----EPKTPDVPKLPDVPKLPDVPK 900
 QY 128 -----FDKVSQK---KIIEEK---DFLVNLSDINAEQSGDFLIRRS 164
 DB 901 LPDAPKLPDGLNKVQAVFTSTGNTKVTVVFDKPTDADKLHLKEVTTKELADKIA--- 956
 QY 165 DDLFYGYVHDNGKLVDAADKFSQYFVVD-----EKRVDNLSDKLTATYRKKEG 216
 DB 957 -----HKTGGGTV-----RVFSLSKGKGKETHVNGERTVRLALQGTGSDV 997
 QY 217 FVYGSNPHTKFAARISKLGDE---IKFENGQAQGSIKDEKGNABIFTIKGDTKQLEI 273
 DB 998 HVY---HVKE-----NGDLERIPSKVGVQV-----FKTNHFSLSFAIKLTSLKQNV 1041
 QY 274 TPTESNRILIIALDONQKSYTPGMEKAIMET---KFDTSKAGN 313
 DB 1042 TPKQOT-----KPSTQGSQVEIASQTGKF-QSKAAN 1072
 RESULT 14
 AAW84461
 ID AAW84461 standard; protein; 1128 AA.
 XX
 XX AAW84461;
 AC
 XX 25-JUL-2000 (first entry)
 DT
 XX Amino acid sequence of a C-beta protein.
 DE
 XX C-beta protein; bactericidal; gram positive bacteria; vaccine;
 KW immune response.
 XX
 XX Streptococcus agalactiae.
 OS
 XX WO200015760-A1.
 PN

Db 1078 TTPKQT-----KPTSGSQVEIAESQTGKF-QSKAAN 1108
 RESULT 16
 AAW40541
 ID AAW40541 standard; protein; 1164 AA.
 AC AAW40541;
 XX
 XX
 DT 28-AUG-1998 (first entry)
 XX
 DE Mutant C-beta protein pnv231.
 XX
 KW C-beta protein; beta antigen; vaccine; group B Streptococcus.
 XX
 OS Streptococcus sp; strain A909.
 OS Synthetic.
 XX
 PN WO9809648-A1.
 XX
 PD 12-MAR-1998.
 XX
 PF 05-SEP-1997; 97WO-US015319.
 XX
 PR 06-SEP-1996; 96US-0024707P.
 XX
 PA (NAVA-) NORTH AMERICAN VACCINE INC.
 XX
 PI Tai JY, Blake MS;
 XX
 DR WPI; 1998-193324/17.
 DR N-PSDB; AAV11348.
 XX
 XX
 PT Group B streptococcal Cbeta proteins - having amino acid substitutions to
 PT reduce immunoglobulin A binding while retaining antigenicity, for use in
 PT vaccines.
 XX
 PS Disclosure; Fig 9A-C; 59pp; English.
 XX
 CC Group B Streptococcus C-beta mutant protein pnv231 has only 60% of the
 CC IGA binding activity of the native C-beta protein (see AAW40537). It is
 CC encoded by mutated C-beta protein DNA (see AAV11348) in which the Lys-170
 CC and Lys-175 codons of the mature C-beta protein coding region are
 CC respectively replaced by a Thr codon and by a Leu codon. These residues
 CC are in the IGA binding domain of the C-beta protein. The IGA binding
 CC ability of C-beta appears to require dimerisation of the protein. The
 CC invention relates to mutant C-beta proteins that have a reduced or
 CC eliminated ability to bind human IGA but which retain the antigenicity of
 CC the wild-type protein. Such proteins can be used in vaccines for use
 CC against group B streptococci. Claimed mutant proteins have mutations in
 CC the IGA binding region of C-beta
 XX
 SQ Sequence 1164 AA;
 Query Match 10.0%; Score 173; DB 2; Length 1164;
 Best Local Similarity 23.3%; Pred. No. 1.7e-05;
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;
 QY 12 TPNHPKVLVPKTONNI-QAQNVPQAQNASQAQNAPOAQNAPQVNAPOAQNAPQ 71
 Db 829 TPDTPKIFELPQADTPQADTPHPSPKAPAPRVPSPKTPAPHPVPSKAPAPR 888
 QY 72 VENAPQAEVTPPVFQ----PQSQKIDGSPDKIGSVKLKNAQTLSELSRFLVDKLTGTPK 127
 Db 889 VPESFKTPAPHPVPSKTPAPKIP-----EPKTPDVPKLPDVPKLPDVPK 936
 QY 128 -----FDKVSQK-----KIIEK--DFLVNLNLSINAELGSDFLIRRS 164
 Db 937 LPDAPKLPDGLNKVGQAVFTSDGNTKVTVVFDKPTDADKLHLKEVTTRELADKIA--- 992
 QY 165 DDLFYGYHDHTNGKLVDAADKFSQFVVYD-----EKRYNDNISKLTATYRKKG 216

Db 993 -----HKTGGTV-----RVFDLSLSKGGKETHVNGERTVRLALGOTGSDV 1033
 QY 217 FVYGSNPHYKEFAARISKLGVE----IKFENGQAQGSINDEKQGNABEFTIKGDTKQLEI 273
 Db 1034 HVY-----HVKE-----NGDLERIPSKVENGQVV-----FKTNHFSLFAIKTLSKQNV 1077
 QY 274 TPTESNRIIAILDQNKSYTTPMEKAIMET---KFIDSKAGN 313
 Db 1078 TTPKQT-----KPTSGSQVEIAESQTGKF-QSKAAN 1108
 RESULT 17
 AAY84462
 ID AAY84462 standard; protein; 1129 AA.
 XX
 AC AAY84462;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of a C-beta protein.
 XX
 KW C-beta protein; bactericidal; gram positive bacteria; vaccine;
 KW immune response.
 XX
 OS Streptococcus agalactiae.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 19 /note= "encoded by TAA"
 FT Misc-difference 23 /note= "encoded by TAA"
 FT Misc-difference 31 /note= "encoded by TAA"
 FT
 XX WO200015760-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-US021643.
 XX
 PR 17-SEP-1998; 98US-0100859P.
 PR 19-JUL-1999; 99US-0144324P.
 PR 15-SEP-1999; 99US-0154017P.
 XX
 PA (NAVA-) NORTH AMERICAN VACCINE INC.
 XX
 PI Long-Rowe KO, Blake MS;
 DR WPI; 2000-271404/23.
 DR N-PSDB; AAA12455.
 XX
 PT Obtaining substantially pure C-beta protein or fragment and/or mutant for
 PT eliciting antibodies which are bactericidal to gram positive bacteria,
 PT useful in vaccines.
 XX
 PS Disclosure; page 131-134; 171pp; English.
 XX
 CC The specification describes a process for obtaining a substantially pure
 CC C-beta protein. The process comprises obtaining the C-beta protein in
 CC cell extracts, subjecting the C-beta protein to ion-exchange
 CC chromatography and collecting the C-beta protein-containing fractions,
 CC pooling and diluting the fractions, and subjecting the fractions to
 CC ligand affinity chromatography and collection. The C-beta protein
 CC fragments are useful for eliciting antibodies which are bactericidal to
 CC gram positive bacteria with complement alone and therefore is useful in a
 CC (combination) vaccine together with a pharmaceutically acceptable carrier
 CC (and/or optionally at least two protein fragments or peptide-
 CC polysaccharide conjugates). The vaccine therefore is useful in a method
 CC for inducing an immune response in a mammal. The present sequence
 CC represents a Streptococcus agalactiae C-beta protein
 XX
 SQ Sequence 1129 AA;

XX	Seq	Sequence 348 AA;
Query Match	9.5%;	Score 165; DB 2; Length 348;
Best Local Similarity	24.9%;	Pred. No. 1.5e-05;
Matches 91; Conservative	54;	Mismatches 140; Indels 80; Gaps 21;
QY	1	CGGGSGGSSSTPHKPKVLVPRKTNNLOAQNVPQAQNASQAQNAPOAQNAPOAQN----56
DB	20	CSGGSGGSSSKPENSE--LTPKVD-----MSAPKAEQ-----PKKEEVPQADNSKAE 64
QY	57	-----APOVENAPOAQN-----APOVENA-----PQAEVTVPVPOQKIDGSPDKIGSVK 103
DB	65	EPEMAPOVD-SPKAEPKNMPOMGNPKLNDPQV-MAPKMDNPQKDAPKE-----E 115
QY	104	LNKEAQTLELSRFTLYDKL-GTPPKFDKVSGKKIIEEKDFL--VLNLSDINAEQLSGDF 159
DB	116	LSKDKSNAILKELGYDINSGLIINNADVVLNLK-IDEKDHITVLDDKGKINRNHLKVTN 174
QY	160	LIRSRDLFGYYHYDTNGKNLVDAADKFQY--FVVYDEKRVNDNISDKLTATVRKKEGF 211
DB	175	TISAQDI-----KTLKDSGKLLGYGYMQLNQVRQDENYSDEKVSF---NEY 220
QY	218	VYGSNPHTKEFAAR-ISKLGDVETKE--NGAOAGSISKDXG-----NAEIFTIKGD 268
DB	221	LLSNMDAKIRPTKSISYKGMFYSDKVGNOQKLKASVEASYDDVTKKVSMKVFGENNDY 280
QY	269	KQI-EITPTESNRILAILDNQOKSYTPGMEKAIMETFKIDSAGNSDQKYLIGEAKSDN 327
DB	281	WKLGEFGTIIINGLYSKIDNFPLKLP-----DANFSGGIFGKNGE-VLAGSAISEK 332
QY	328	WQAIM 332
DB	333	WQVI 337
 RESULT 19 ABBS8463		
ID	ABBS8463	standard; protein; 837 AA.
AC	ABB58463;	
DT	26-MAR-2002	(first entry)
DE	Drosophila melanogaster	polypeptide SEQ ID NO 2181.
XX	Drosophila;	developmental biology; cell signalling; insecticide;
KW	pharmaceutical.	
OS	Drosophila melanogaster.	
EN	WO200171042-A2.	
PD	27-SEP-2001.	
PF	23-MAR-2001;	2001WO-US009231.
FR	23-MAR-2000;	2000US-0191637P.
FR	11-JUL-2000;	2000US-00614150.
XX	(PEKE)	PE CORP NY.
PI	Venter JC,	Adams M, Li FWD, Myers EW;
XX	WPI;	2001-656860/75.
DR	N-FSDB;	ABEL02566.
XX	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.	
PS	Disclosure;	SEQ ID NO 2181; 21pp + Sequence Listing; English.
XX		


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XX 01-JUL-2004.
PD
PF
XX 16-DEC-2003; 2003WO-EP051019.
XX
PR 17-DEC-2002; 2002EP-00102781.
PR 12-JUN-2003; 2003WO-EP050222.
XX
PA (CRUC-) CRUCELL HOLLAND BV.
XX
PI Pau MG, Holterman L, Kaspers J, Stegmann AJH;
XX
DR WPI: 2004-488068/46.
DR N-PSDB; ABQ30502.
XX
PT New replication-defective recombinant viral vectors having a heterologous
PT nucleic acid encoding an antigenic determinant of Plasmodium falciparum
PT or yoelii, useful for developing vaccines against malarial infections.
XX
PS Claim 18; SEQ ID NO 9; 94pp; English.
XX
CC The invention relates to a replication-defective recombinant viral vector
CC comprising a heterologous nucleic acid encoding an antigenic determinant
CC of Plasmodium falciparum or Plasmodium yoelii, where the nucleic acid is
CC codon-optimised for elevated expression in a mammal. The methods and
CC compositions of using recombinantly produced viral vector as a carrier of
CC an antigenic determinant from malaria pathogens for the development of a
CC vaccine against malarial infections. This sequence corresponds to the
CC protein encoded by a codon-optimised circumsporozoite gene from
CC Plasmodium yoelii.
XX
SQ Sequence 356 AA;
Query Match 7.6%; Score 131; DB 8; Length 356;
Best Local Similarity 36.0%; Pred. No. 0.013;
Matches 32; Conservative 3; Mismatches 54; Indels 0; Gaps 0;
QY 2 CGSGSGSSSTPNHPKPVLPVKTQNNLQAQNVPOAQNAPQAQNAPOAQNAPQVE 61
DB 154 GAQPGGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 213
QY 62 NAPAQNAPOVENAPQAEVTPVPQPSQ 90
DB 214 GAQPGGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 242
RESULT 24
AAB07288
ID AAB07288 standard; protein; 478 AA.
XX
AC AAB07288;
XX
DT 17-OCT-2000 (first entry)
XX
DE Human IL-2/ P. yoelii circumsporozoite protein (PycSP) fusion protein.
XX
KW pDIP/PycSP.1 plasmid; malaria vaccine; circumsporozoite protein;
XX protozoacide; immunoenhancer; human; rat.
XX
OS Plasmodium yoelii.
OS Homo sapiens.
OS Rattus sp.
XX
PN US6066623-A.
XX
PD 23-MAY-2000.
XX
PF 23-NOV-1993; 93US-00155888.
XX
PR 23-NOV-1993; 93US-00155888.
XX
PA (USNA ) US SEC OF NAVY.
XX
PI Sedegah M, Hoffman SL, Hedstrom RC;
XX
DR WPI: 2000-410681/35.
DR N-PSDB; AAA58309.
XX
PT Inducing protective immune responses against Plasmodium parasite proteins
PT for controlling malaria in mammals comprises injecting a polynucleotide
PT delivery vector having a DNA sequence coding for the Plasmodium protein.
XX
XX Example 1; Col 21-24; 2ipp; English.
XX
CC The present sequence is the protein sequence of human IL-2/ Plasmodium
CC yoelii circumsporozoite protein (PycSP) fusion protein. This protein is
CC encoded by the plasmid vector pDIP/PycSP.1 (AAA58309). The expression of
CC this protein results in the production of an immune response to the
CC malaria protein and a reduction in malaria parasites at the pre-
CC erythrocytic, erythrocytic, and gametocyte stages of infection. The
CC plasmid encoding the present sequence can therefore be used as a malaria
CC vaccine. The present sequence also has a partial rat preproinsulin II
XX
SQ Sequence 478 AA;
Query Match 7.6%; Score 131; DB 3; Length 478;
Best Local Similarity 36.0%; Pred. No. 0.02;
Matches 32; Conservative 3; Mismatches 54; Indels 0; Gaps 0;
QY 2 CGSGSGSSSTPNHPKPVLPVKTQNNLQAQNVPOAQNAPQAQNAPOAQNAPQVE 61
DB 265 GAQPGGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 324
QY 62 NAPAQNAPOVENAPQAEVTPVPQPSQ 90
DB 325 GAQPGGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 353
RESULT 25
AABU02252
ID AABU02252 standard; protein; 4365 AA.
XX
AC AABU02252;
XX
DT 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX
DE S. pneumoniae type 4 strain protein from coding region #1830.
XX
KW Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
XX antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
XX Gene therapy; vaccine.
XX
OS Streptococcus pneumoniae; type 4 strain.
XX
PN WO200277021-A2.
XX
PD 03-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-IB002163.
XX
PR 27-MAR-2001; 2001GB-00007658.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Masignani V, Tettelin H, Fraser C;
XX
DR WPI: 2003-040579/03.
DR N-PSDB; ABX07542.
XX
PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
PT ear infection.

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XX Claim 1; SEQ ID NO 3660; 56pp; English.

PS The invention relates to a protein comprising or having at least 50%

XX identity to any of the 2469 amino acid sequences, identified in the

CC specification (available on a computer readable format), or its fragment,

CC expressed from 2469 of 2489 identified DNA coding regions from the

CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as

CC AS55454. Also included are an antibody which binds one of the proteins,

CC treating a patient by administering the protein, DNA or antibody (in a

CC composition), a kit comprising first and second primers, which are the

CC nucleic acid cited above or fragments between nucleotides 8-100 of a

CC sequence not defined in the specification, for amplifying a target

CC sequence contained within a Streptococcus nucleic acid sequence, where

CC the first primer is substantially complementary to the target sequence

CC and the second primer is substantially complementary to the complement of

CC the target sequence, and where the parts of the primers having

CC substantial complementarity define the termini of the target sequence to

CC be amplified, assay comprising contacting a test compound with the

CC protein, and determining whether the test compound binds to the protein.

CC and a Streptococcus pneumoniae bacterium, where one or more genes

CC encoding the proteins has been rendered inactive. The proteins, nucleic

CC acid molecules, antibody and compositions are useful as medicaments for

CC treating or preventing a disease or infection due to streptococcus

CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis

CC media or ear infection. They are also useful in developing vaccines,

CC diagnostics and antibiotics. The methods are useful for identifying

CC immunodominant proteins. The present sequence is one of the 2469 proteins

CC expressed by the identified coding regions from the genomic sequence.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to

CC standardise OS field)

XX SQ Sequence 4365 AA;

Query Match 7.5%; Score 129.5; DB 6; Length 4365;

Best Local Similarity 38.1%; Pred. No. 0.57; 23; Indels 29; Gaps 4;

Matches 37; Conservative 8; Mismatches 29;

QY 18 PVLVPTKQNNLQAGN--VPOAQNASQAQN-----APQAQNAPOAQ 55

Db 36 FVLQSQQQVLPQHRQVRLQQAQHLNQRQVLRQLQVPLQLQHQPAQRQAPQLL 95

QY 56 NAPIQVNAPOAQNAPOVNAPOAEVTPPPVQPSQKI 92

Db 96 NRPG--PAPRPQAPQLLRPQ-----PAPQPQHQRV 125

RESULT 26

ADM16778

ID ADM16778 standard; protein; 448 AA.

XX AC ADM16778;

XX DT 03-JUN-2004 (first entry)

XX DE N. patriciarum xylanase #1.

XX KW xylanase; food; feed; pulp industry; paper industry; enzyme.

XX OS Neocallimastix patriciarum.

XX FN US2004053238-A1.

XX PD 18-MAR-2004.

XX PF 17-SEP-2002; 2002US-00244596.

XX PR 17-SEP-2002; 2002US-00244596.

XX PA (HSEU/) HSEU R.

XX PA (HUAN/) HUANG Y.

XX Hseu R, Huang Y;

XX WPI; 2004-327305/30.

XX New recombinant thermo- and alkaline pH-tolerable xylanases derived from

PT anaerobic fungi, useful in a number of applications e.g. in the food,

PT feed, and particularly in the pulp and paper industries.

XX Example 4; SEQ ID NO 14; 48pp; English.

XX The invention relates to a xylanase or its xylanolytic fragments. The

CC methods and compositions of the present invention are useful in a number

CC of applications in the food, feed, and particularly in the pulp and paper

CC industries. The present sequence represents the amino acid sequence of a

CC N. patriciarum xylanase.

XX SQ Sequence 448 AA;

Query Match 7.3%; Score 127; DB 8; Length 448;

Best Local Similarity 36.8%; Pred. No. 0.041;

Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4;

QY 2 GSGSGSGSSPTNPKPVLVPTKQNNLQAGNVPQAQNASQAQNAPOAQNAPOV 61

Db 240 GGAPAGGAPAGNDPQG---PQGQPPQGGPPQGGQPPQGGQPPQGG-NDQGGQ 295

QY 62 NAPIQVNAPOVNAPOAEVTPPPVQ-POSQKIDGS 95

Db 296 QPPQGGQPPQGGNDQGGQ-QPPQGGQPPQGGNPGGS 329

RESULT 27

AAW65462

ID AAW65462 standard; protein; 485 AA.

XX AC AAW65462;

XX DT 17-OCT-2003 (revised)

DT 09-NOV-1998 (first entry)

XX DE Neocallimastix patriciarum endo-xylanase.

XX KW Endo-xylanase; xynC gene; transgenic plant; Brassica napus; oilseed rape;

XX canola; feedstuff.

XX OS Neocallimastix patriciarum; strain 27.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT /label= Sig peptide

FT /note= "putative signal peptide"

FT 21..485

FT /label= Mat_protein

XX PN CA2190194-A.

XX PD 13-MAY-1998.

XX PF 13-NOV-1996; 96CA-02190194.

XX PR 13-NOV-1996; 96CA-02190194.

XX PA (LIU/) LIU J H.

PA (SELI/) SELINGER L B.

PA (MOLG/) MOLONEY M M.

PA (FORS/) FORSBERG C W.

PA (CHEN/) CHENG K.

PA (HUYU/) HU Y.

XX PI Liu JH, Selinger LB, Moloney MM, Cheng K, Hu Y, Forsberg CW;

XX WPI; 1998-428424/37.

CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

PT Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used to induce protection against disease caused by transferrin producing PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.


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DR WPI; 2001-639362/73.
DR N-PSDB; AAS80423.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 46595; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridization probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 930 AA;
Query Match 7.2%; Score 124; DB 4; Length 930;
Best Local Similarity 20.8%; Pred. No. 0.2;
Matches 80; Conservative 65; Mismatches 141; Indels 98; Gaps 19;
QY 2 GSGSGGSSSTPNHFKPVLVPTQNNLQAVPQANASQAQANAP-----QAQNAPOAQN 56
DB 225 GLSAYDNSRSPHSPSPATPSSQSS-SCSDAPMLSTVHSKNTSPSHSHSIQSPERSG 283
QY 57 APQVENAPQ-----AQANP-----QVENAPQAVTTP-VPOPOSQKIDGSPDKIGSVKLKE 107
DB 284 GSGVNGSSRYSPSONSPIHIHPRRSPAKTIAPQNAPRDESGRKSRFPDGGQETAKT 343
QY 108 AQTL-----ELSRFTLVKLTGTPPKFDKVGKIIIEKDFVLVNLSDINAEQLSGDFLIR 162
DB 344 GKFLKRFYDESRVFLLDGRNTR---DKEASKEKSEKG-----RAEGEWEDQ 388
QY 163 RSDDLFYGYHDNGKLVDAADKPSQVYVYDSEKRVNDNTSKLTAT-----YRK--- 214
DB 389 EALDYF-----SDKES-----GKQFNDSGDDTEETDYRQFKSVLA 427
QY 215 ---EGFVYGSNPTKE---FAARISKLGDVE-----IKFENG---QAQGSIKD 253
DB 428 DQKSFATASHRNTEEGLYKSKVSLKGNRESGDFREEKYKLG-ETGYVVERSPSTTKD 486
QY 254 ---EXDGNAEFTIKGDTKQLEITPTESNRIIAI-----LDQNKSYTPPGMEKAIM 303
DB 487 KHKEEDKNSERTVKKETQSPQVKSEKLGKLDLFVSPPLHKNLDAAREK--TFREESPLR 544
QY 304 TKFIDSKAGNSDKVLIGEASDN 327
DB 545 IKMTASDSHRPEVKLMAPVFLDD 568
RESULT 39
ABB59487
ID ABB59487 standard; protein; 861 AA.
XX
AC ABB59487;
XX
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DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 5253.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
DR WPI; 2001-556860/75.
DR N-PSDB; ABL03590.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 5253; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 861 AA;
Query Match 7.1%; Score 123.5; DB 4; Length 861;
Best Local Similarity 27.7%; Pred. No. 0.2;
Matches 38; Conservative 15; Mismatches 61; Indels 23; Gaps 3;
QY 2 GSGSGGSSSTPNHFKPVLVPTQNNLQAVPQANASQAQANAPQANAPQANAPQVE 61
DB 641 GVSAGQCTAQIKPKPKP-----RAPRVKPKPKPKPKPKPKPKPKPKPKPK 690
QY 62 NAFQANAPQVENAPQAEVTPPVPOPOSQKIDGSPDKIGSV-----KLKAEQTL 114
DB 691 KAPRVKAPRVKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 744
QY 115 RFTLVKLTGTPPKFDKV 131
DB 745 RAPRVKPKPKPKPKPKPK 761
RESULT 40
ABU35643
ID ABU35643 standard; protein; 599 AA.
XX
AC ABU35643;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #21170.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
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OS Mycoplasma genitalium.
PN WC20027183-A2.
XX
XX
PD 03-OCT-2002.
PF
PF 21-MAR-2002; 2002WO-USC09107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 05-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Irawick JD, Carr GS, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA39513.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 63567; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 599 AA;

Search completed: December 17, 2004, 15:56:30
Job time : 209.087 secs

Query Match
Best Local Similarity 7.0%; Score 122; DB 6; Length 599;
Matches 54; Conservative 44; Mismatches 75; Indels 70; Gaps 13;
16 PKPVLVPTKQNV-PQANASQA-QNAPQANAPQNA-PQENAPQANAPQV 72
317 PKPVLVPTKQNV-PQANASQA-QNAPQANAPQNA-PQENAPQANAPQV 370
73 ENAPQAEV-----TPPVQPOQKIDGSDFKIGSVKLNKEACTLELSRFTLVDX 121
371 ESTPQVEVHHWKEVKEVQPPQPLFTS-----GLQKIVPSPAALLQSK 415

Query
Db
Query
Db

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